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Zavras

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- (54) **PHARMACOGENETIC TEST
ANTI-RESORPTIVE THERAPY-ASSOCIATED
OSTEONECROSIS OF THE JAW**
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C12Q 1/68 (2006.01)
C07H 21/02 (2006.01)
C07H 21/04 (2006.01)
- (52) **U.S. Cl.**
CPC *C12Q 1/6883* (2013.01); *C12Q 2600/156* (2013.01); *C12Q 2600/172* (2013.01)

(58) **Field of Classification Search**

None

See application file for complete search history.

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(57)

ABSTRACT

The present invention relates to methods and compositions for testing individuals to determine whether they are at increased risk of developing anti-resorptive therapy-associated osteonecrosis of the jaw.

5 Claims, 27 Drawing Sheets
(10 of 27 Drawing Sheet(s) Filed in Color)

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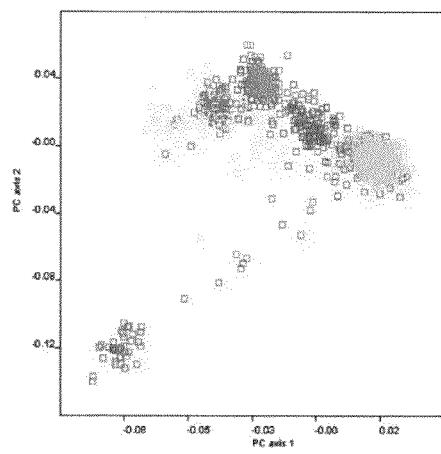
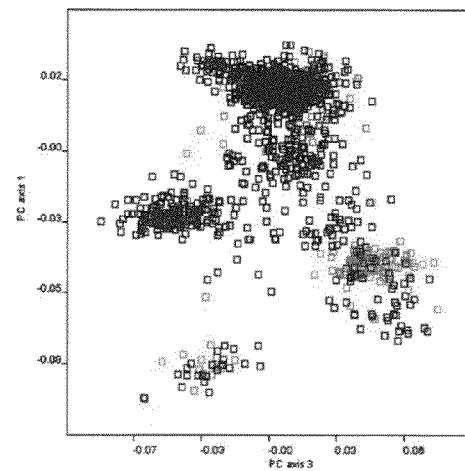
Figure 1A-B**A.****B.**

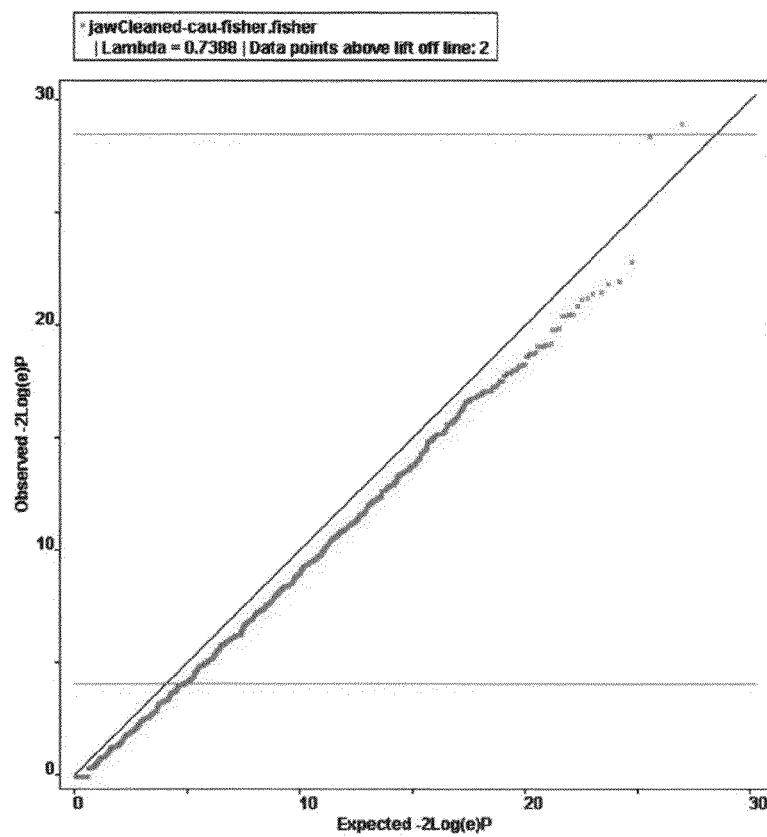
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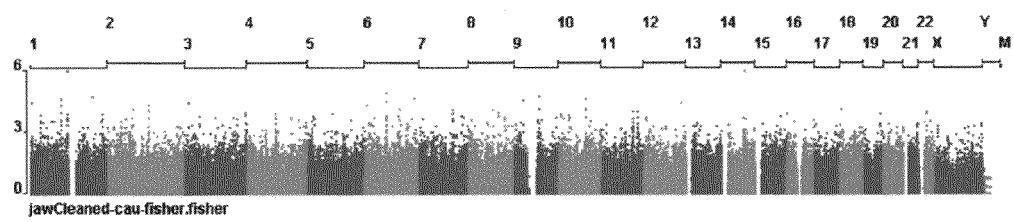
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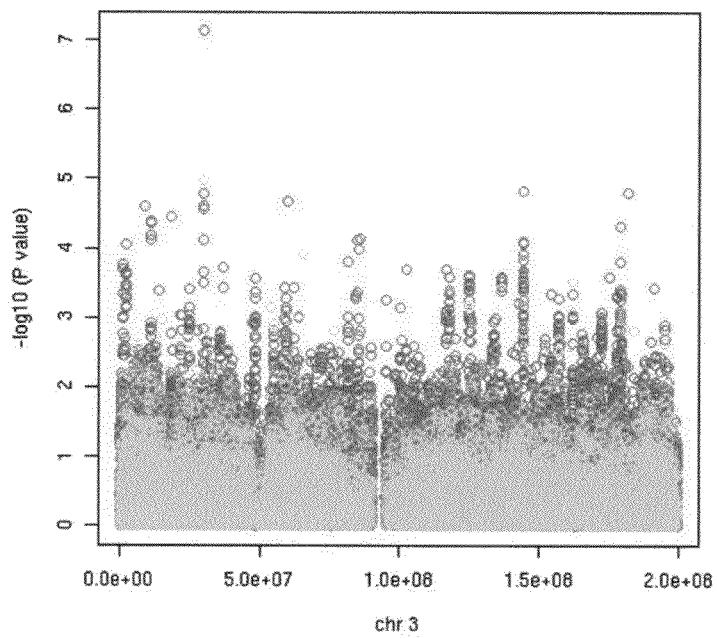
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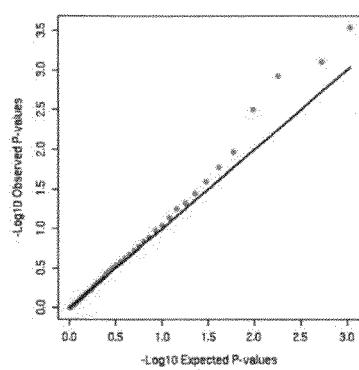
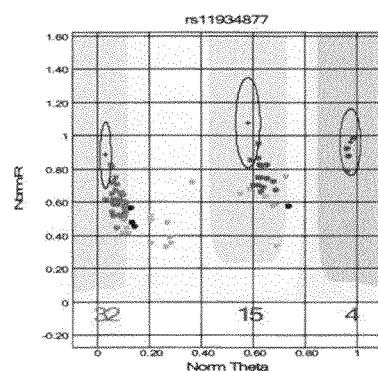
Figure 5A-B**A****B**

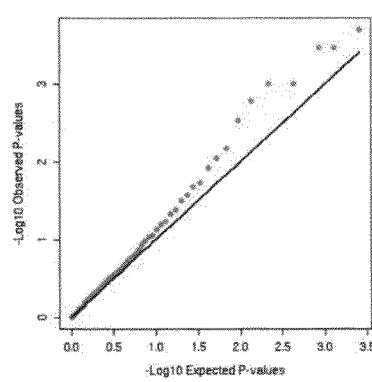
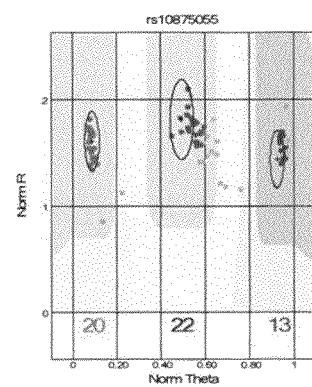
Figure 6A-B**A****B**

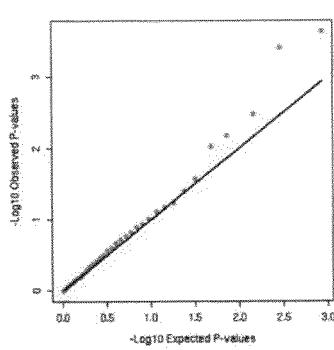
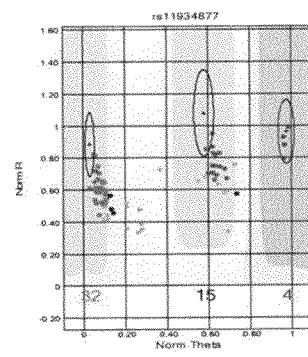
Figure 7A-B**A****B**

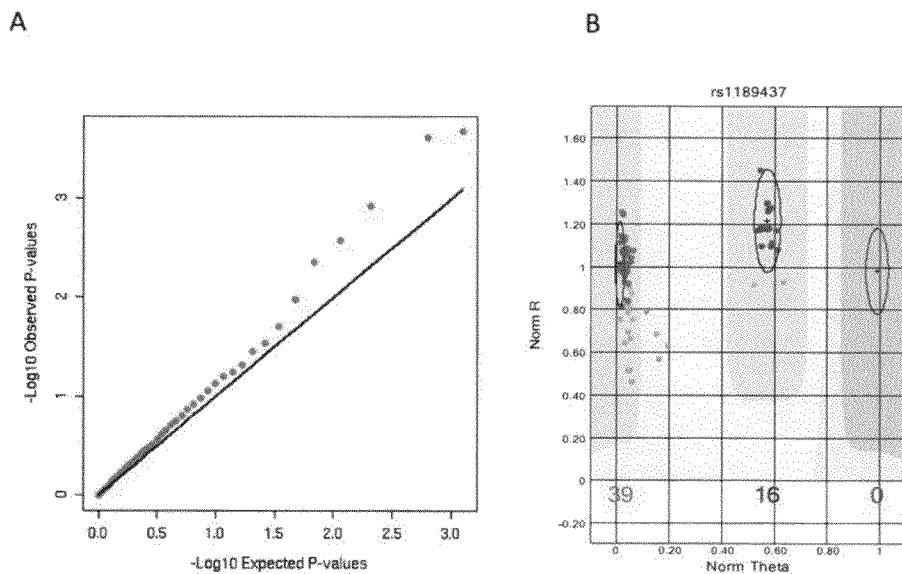
Figure 8A-B

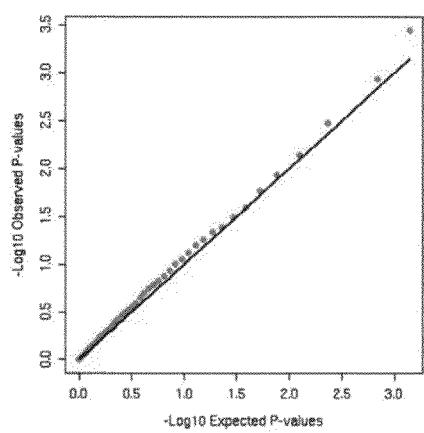
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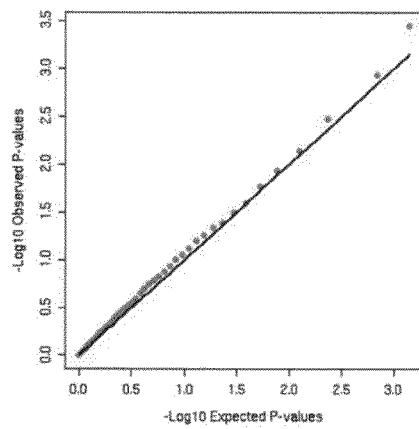
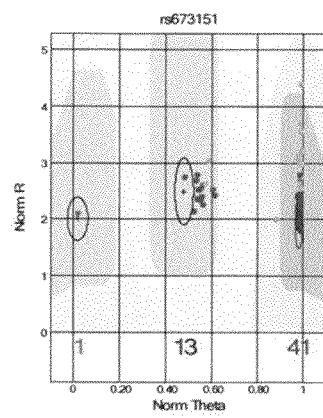
Figure 10A-B**A****B**

FIGURE 11A

618421 ccggccatcag ttatgcAACC aacagtaacc aatattttca
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 618601 aaggcatgAC aatagatAGC tagagatCAA catagacATA gaatcAGATA aaggagAGG
 618661 gtgaaaaAGC aagagAGGT gagaGAGGA gaggAGGAGA gggaaACTTA tttagaaGAAA
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 619861 caggctcacAC ttttttttttG gatgtGCCTT aggggacaATT
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 620341 gtacttttttG ttttttttttG gatgtGCCTT aggggacaATT
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 620461 taatgttttG gggctggggGT gtttttttttG gatgtGCCTT aggggacaATT

FIGURE 11B

FIGURE 11C

FIGURE 11D

FIGURE 11E

627001 tctgactgtt gcatagttga tagtcatgtt gctgaatgtat caaatcaatc ggattgtgaa
 627061 atgcacagg cttaacaaaa ttagccatatt ctttgctcc atgactagt tttgtataatt
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 629101 gttgaatgtt tggatgttcat gatcagaaaac gggtttccat attggggatgtt

FIGURE 11F

629161 ttctcaaatg tgaagagtagc atctcaaaatg taatccaaaatg gatattttat ttgattttttt
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629701 acaaataattt ctaatatgtt catctatggt taacagttaa ggtatgtca aagtctataaa
629761 gctgttaaaga ggagggaaatggt actctatgtg gggggatgtg agggatgtgg acaaagggtttc
629821 acaggagggg taacttcctgtactgtttt gttttttttt tagaccaacaa
629881 agtgtgggt gtccggcagg aagggtgtc tgagcaaaatgt gatcgtatggat ttgttagggcag
629941 ggtttggc cttttttttt cttttttttt cttttttttt cttttttttt cttttttttt cttttttttt
630001 ttttacggc taccagggtc ctattccacca tggtgtcgat ctgggtttttt cttttttttt
630061 caacatgtt gcacacaaatggt gttttttttt cttttttttt cttttttttt cttttttttt
630121 attaaacatg gcatctttttt cttttttttt cttttttttt cttttttttt cttttttttt
630181 aatccatgtt gttttttttt cttttttttt cttttttttt cttttttttt cttttttttt
630241 tgttatgtt atactttggg tttttttttt cttttttttt cttttttttt cttttttttt
630301 tagtctaat tttttttttt cttttttttt cttttttttt cttttttttt cttttttttt
630361 aagaatgtgtt agtgtctcat cttttttttt cttttttttt cttttttttt cttttttttt
630421 aacaataaaatggatgtataa gttttttttt cttttttttt cttttttttt cttttttttt
630481 gagttttttt ttctatgtg tttttttttt cttttttttt cttttttttt cttttttttt
630541 tagacttaga cttttttttt tttttttttt cttttttttt cttttttttt cttttttttt
630601 tcataacaatggatgtt aaaaatggatgtt cttttttttt cttttttttt cttttttttt
630661 atacataataa gcttagatgtataa tttttttttt cttttttttt cttttttttt cttttttttt
630721 tgatgtatggatgtt tttttttttt cttttttttt cttttttttt cttttttttt cttttttttt
630781 atgggtggc aatataatggatgtt tttttttttt cttttttttt cttttttttt cttttttttt
630841 tctttttttt cttttttttt cttttttttt cttttttttt cttttttttt cttttttttt
630901 ttctccgt tttttttttt cttttttttt cttttttttt cttttttttt cttttttttt
630961 attttgcattttttt cttttttttt cttttttttt cttttttttt cttttttttt cttttttttt
631021 acaaagggtttt cttttttttt cttttttttt cttttttttt cttttttttt cttttttttt
631081 agggaaaatggatgtt tttttttttt cttttttttt cttttttttt cttttttttt cttttttttt
631141 tgtcgtatggatgtt aaaaatggatgtt tttttttttt cttttttttt cttttttttt cttttttttt
631201 sttttcaat tttttttttt cttttttttt cttttttttt cttttttttt cttttttttt
631261 cagcgatgtt tttttttttt cttttttttt cttttttttt cttttttttt cttttttttt

FIGURE 11G

631321 tcttttattta actctcaata aaaggccaagg acatgttaac tttcaattttt ctgaagaat
631381 gtbabggca actacattaa tattttcag gtatgttaagt ttatccatcac
631441 ataagaatga ctcagtaaat ccaatttgct gacatgtggc ttattttttgtt
631501 ctgaggcagg atgttattaa atttatacca tctgtatttt agtttcaccc aggtacaggc
631561 tattttactt ctcattggaa agatggcaag atttttccatc
631621 ataaatgtct tc当地tgc当地 agtggcaat tttttttttt
631681 tctgtgtgtg agaggcaat cttttttttt
631741 acctttggc taatcatcaat aggtggctca taaatgtactc
631801 cbctgtatgc ctgtccaaat tgaatcagggt gt当地tgc当地
631861 ctgtatagaat agaaacttttt gatgtggacc atggaaatttt aaaaatgtatc
631921 atgatttggc atc当地tgc当地 aaccatctta ttcttacaata attacttaat
631981 atgtttagca gactctgtt gaaatgtgca gaaaaacttat atcatcgca
632041 gagaaaacat ctctttgtg accitggag ggatccaaat agtttcagggt gcttcacact
632101 gttttatggcat aatatttttgc aatatttttgc aatatttttgc
632161 taatgtataat ttcatatggc aatatttttgc aatatttttgc
632221 aaagccaaattt ccaagaaaaga ggatgttcc ttatctatgt gaaatggat
632281 tggctttttt ttctttttttt gcatagggaa aatccaaatgtt
632341 ataataaacct taaaacttctt atttggaaaga gaaaacctttt atccaaatggat
632401 cggbbtttaa tcaatcacca ttggaaacat ttcttgccatcaaa caatgttgta tatttttttt
632461 caatttttttcc ttcccgatcaa aggcttttat cttgttttgtt atcttcaatc
632521 aatactggaa aatccattat gtttccaaatgt ttgttgttaca tgatcatatgt
632581 agatttotgt atccacactcc aaaataatct aacttttcttga gatgtatata
632641 ttcaaggaaat ttgttttattt atacatggca tgaactgtatg aatgtttttt
632701 tacacattac tgccatata tgaccctccat tabatattt atttaaacaa
632761 aagactgaca tatacatat atacaatgtt gtgtttttat ggggttattc aggttttacat
632821 tttaaggactg aacactgttg agattttgtt tattttttatg taaggaaagaaat
632881 atggatgggtt caaaactgac tcggaaat ttccatgttgg
632941 tcctttaaactt gaatttaggtt gtgttggatggaaaggaaatggatgggg
633001 ttcccttttgg gcatgttgac ttttcaaggc cagataaaaga ttttcaatat gtagatccaa
633061 atacaggttt gcaccccaag aagggtatgtt ataaactttt ggttcatatca
633121 agatataca tggatgtt agcaatttcgc tcacttttca tagtaattac
633181 ctatgcaata gctatgtgtg tgccatagctt gagggttaccc taaatttttat
633241 gtactaaattt aatgttttgc atatgtttgc tttttttttt
633301 tgctttttttt tataccctata ctgtttatggc taatctatgtt tttttttttt
633361 tgaatataatc aatgtatat gcaatgtatg tttcccttttta
633421 agtttagggaaat atagagatac ttccaaattttt aagaaatctt agggcccccc
aatgaatgtt

FIGURE 11H

633481 agcggtttagt gtaaagggtt cagaatttgtt cctgtgtatc catgeaaaaac tgtttcattt
633541 cccattttgc aacatttcg gaaacttttt ttatattaaat tttttttttt ccataggcc
633601 tagccccgtt agtggaaaga caacaaaaatt ggaaaaggcac agcaacaagg ctctgtctag
633661 taaaaccaa gaaagcaata aacccttgcc aacccttataa gaaaaattta aaagtccacc
633721 gtttattttat cttgttgtt agatataatct gtcttcattgt taatgttcattt gtaatgcagg
633781 gatrttataaa cccttactacta ttatctactgg agggtttccca cttttttttt aatagagtgt
633841 tcddttaaaaa aaaaaatctc attttttttt ctttttttgc aagaatataat tattttcaggc
633901 ttgtgtggat atccctatct ttggccctttt gggctttttt ccgtttttttt ctcttaacgtt
633961 ctgggtatc ttggtaatga ctgggtatc ttggtaatga gaaatgtatga gctcagagg
634021 actctactaat tcctaatgtgt ttccaaatggc caactttgaaa aatgtatca gggggatgtg
634081 agggcttaat tactgaagac catctatgtt ttctgtgggg tttttccatgg ccctgtatatt
634141 gtttacatgt ttttttttttt gttttttttt ctctgtttttt ttgtacattt taaaggcag
634201 aaggtttaag taagttttttttt aagaatccgt aacagtatcgc ccgtatctc agacaatgt
634261 ttccaaatgtt gattgtggct caaagattttt acttttccccc atgttctttt ctaaatacaa
634321 agttccaaacc gaaattgtca agatgtggaa ttcatattgaca gacatcagc agggatcc
634381 tttagtggaa tattacccgtt gataaaaaag gataaaaaat ttccaaatataa aacctttaat
634441 ctgtgtctatc taattactgtatc aatctgtatc aatctgtatc aatctgtatc tttttcatctt
634501 ttgtgtttttt aacaaagaaa agaaacaaa aacgttaattt tgcattttttt tgatctgttggaaaactt
634561 aatgtccaaatg ctatgtatct tagtcttttcc ttcttgatgtt gacttggatggatggatggat
634621 attttctgtt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
634681 aatgttatgtatc gatctgtatc tttttttttt tttttttttt tttttttttt tttttttttt
634741 ctatctacaca ttgttcaggca tatgttggaa tttttttttt tttttttttt tttttttttt
634801 aacttgtccca gaaaatgtta tttttttttt tttttttttt tttttttttt tttttttttt
634861 atgtggggat gaaaggccctt ctactttttcc ttcatatccctt gttttttttt tttttttttt
634921 ttctttttttt cccctctcc attttttttt gttttttttt tttttttttt tttttttttt
634981 ttacttaattt acctcatat attgtctttttt tttttttttt tttttttttt tttttttttt
635041 ttaataatct cctgtatcata tttttttttt tttttttttt tttttttttt tttttttttt
635101 ttaaaaatgtca ttgtttttttt tttttttttt tttttttttt tttttttttt tttttttttt
635161 ttgtttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
635221 gcagggrgtt aattatctatc gaaaacttacc tttttttttt tttttttttt tttttttttt
635281 tccttataagca ggcttcttaat tttttttttt tttttttttt tttttttttt tttttttttt
635341 agttaaggag accaaaaat atgtgggttg tttttttttt tttttttttt tttttttttt
635401 atacggaaaca ttgtggattttt tttttttttt tttttttttt tttttttttt tttttttttt
635461 ttcccttaggg gaaagaaaaac ttgtttttttt tttttttttt tttttttttt tttttttttt
635521 ttgtggaaagaa ttttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
635581 ttgtttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt

FIGURE 11K

639961 caggctggtc aggaactcct gaccctaagt gatctgctg cttcagccctt ccaaactgt
640021 gggattacag acatcgagcc gcagcacitg gtttaacctt ttataaaa
640081 cccactatacg tcagaataatgc cactcagaat atgtgggtta gctgaatttg ctatcccatt
640141 gccatcaaaa ttctaaaaagg tatccaactga cagactgttt ggcagggggg tgggggggct
640201 ggggtggcg caaaaatagt caggaggaat gacacaataa aatattacca atccaatcaac
640261 cagtggatgc acaaactggcc ttgatcagg ctaaggagaa aggggggtctc ccctataatg
640321 agctgtgatt aacaacacgaa attaccggaa tgaatttca gcaactctt cagagatgag
640381 ccatccatgc cttagactt ctttgcactt ctttgcactt gtaaagatag ggatattttt gtttttgtatt
640441 actaagataa caatttgcgca atgttttag atgcataatccg gtgtgttctac aaggccctcat
640501 catattttag agtttttcc ttccctacatgt atgttttca gcttgataact cagtgtatcc
640561 aggttatttcc ctggggaccc agggcccttct gcttgaaagcaa aacatccagg cttgtctcaac
640621 atagacatgtt ctttactta ctttgcactt ctttgcactt tgtaaagatag ggatattttt gttgtacttca
640681 ggagtgtgat ggttagtagca tcacccatgt aaaaatttca actaaaaaaa agacagaaaa
640741 tgacatggca tctccaataa tgtttacttt tgtaatcttc ttgattttactt
640801 tatattgtat ttgtgaaact tacttattta tagttttta aagtatttta actgttaattt
640861 atcttcgtat ttttcacag caagatataa ctttgcactt ctttgcactt tggtttttt
640921 aatcccgaca ctgggggg ccgggggg tggatcatga ggtcaggaga tcgagaccat
640981 cctggtaac aaggtaaac cccgtctcta ctaaaaatac aaaaatttgcgggggg
641041 tggcgggcgc ctgttgtccc agctactgg ggggtgggg caggagaatgg gctgtgaaccc
641101 gggaaaggaa gctttcaatgt tgccgactgtc agtccgcactgc agtccgcactgc
641161 cgacagagcg agactccgtc taaaaaaaaaaa aaaaaaaaaa gatagaaaaact
641221 cagcatbtcg gaatgtatga attatgtat attctttttt ctaaacactg tacagtacca
641281 aaatattttt taaaatgtat tgaatgtat tttttttttt tttttttttt
641341 taatttgcgt acccccttcgt tattttcaatgt tgacacaattt ttttttttt
641401 ttatcaatt tcaaggccagc taagatagac ttctttttttt
641461 aaaaatatat cttaatatca gggattttttt tttttttttt
641521 tccatataaa acaaataatgt tttttttttt
641581 ggggtgtaaa cattccctcg tttttttttt
641641 catactaaa ctaactgtat tttttttttt
641701 cacatgtat atgtttcat tttttttttt
641761 tgaccgtgtaa gggttttttt
641821 ctgtgtttaga gggaggcccttac tttttttttt
641881 ttgttttttcc ttgtgtttttt
641941 gccacatgtt acaatggggc tttttttttt
642001 agataaacta gcaatggggc atagatgtataa tttttttttt
642061 aaacaacgtt cttttttttt atgtgtgttataa tttttttttt
642061 aaacaacgtt cttttttttt atgtgtgttataa tttttttttt

FIGURE 11L

642121 taggaatgaa agatgtgttgg ttggggggca gatggttcca ggcttttgtct tgcatggaaat
 642181 aaagccaaag tatgtttaa aaatcttcga cagtgtcaa gtcatgtatc ttggcgacc
 642241 gttcacattcc ttgcctatcc catgtgtatc aactggggat gaaaaggggat tgcttagggaaa
 642301 aaataaatggc agaaaaaaa aactgggttct gaataattttt tttttttggat acttttaatac
 642361 atcagtataa tttaaactgg aggctggag gtcaaaaaaaaaac gtgtttttgtc aataaggtttc
 642421 tttaaatat tatgtatccc atgtttttttt ttatagaatg tttgtttaagg aataaaaaaa
 642481 tgctatgtca ccaaggccat ataatgataa atatttccaa tgtgaaatccc aatttgataga
 642541 cataaagtcc tatttgttcc tgtaaaggaa gcaatggggaaaataaaaaggatcataaata
 642601 aactattttt gatgtbaatta taatagtttt gtttccacc ccacatgtct tcgaaaataaa
 642661 attaaaaaca ataaatcta catacgtttt tatttcataa agtgtctata gaaaaggaaa
 642721 tcttttgcac agacaaactgg attgtcaataa aatgccgaat attcttgcac aatacaattc
 642781 tataatacc ctgttacatg accaaagggtt accactgtca cttgttgtcc ccaaaaccatt
 642841 ccactctgtct aatgttgcac attgttgcac actgtgtgc actgtgtgc actgtactttt
 642901 gcccccaacc cacccggaaaa atggatgtca cattccttgc tcattttttt ttttaatctg
 642961 tcttttcaact ctaattccct tgcagggtgtct tttgtattttc aatcttatatc
 643021 tagcagccaaa agggtttagt aatgtttagt tttttttttttaatcattttttt
 643081 cttttttttc atttctcacat tgaagaggta ggttacacac tggggggaaaaac taatgacatc
 643141 tgaagagagt attaaaaat aaattttcac atccatgcatttgcatttttc taaggatct taagaaaga
 643201 agcaactgg atggtccaaat atcccccggccaa atgggggaaa taaggatcttcc
 643261 tcacggccgtat atccccggccaa atggggggggccgc
 643321 tcaaggaccat octgatcaac atggggggggccaa
 643381 aggtgtgtgt gtgcgtgcgttcc atatccgg
 643441 ttggacccctgg gggggggaga ttgcgtgtgag ccaagatcac
 643501 gccaacaaggatg ggg
 643561 gaaacgattt aaaaaaaaatttttgcgtgtgtgt
 643621 ggtgtgtgt gtggatgg
 643681 atcgccggat ggg
 643741 acatgtgtat ttgggggtac atggggatttttttttgc
 643801 cgg
 643861 gcaatgttgc ttaatgtgtat ggg
 643921 ttttttttttttttttttttta ttt
 643981 totatggggc atataaccatc ttt
 644041 ggttaaggatg atgacgtttat ttgg
 644101 aatatgtgtat ggg
 644161 ggg
 644221 aaggagttat attaaatatta ctaattatc tccaaatatttccat ctttttttttttttttttttt
 agcaagaaca

FIGURE 11M

644281 aacaaaggac ttaacaaaat gattgaggt caaaccaaga atcttttttag aagcaatgtt
644341 atagaaaaatt cactcagac cctggcagc cttttttttttt ccaaaggcttta
644401 tcgtgaaat aactcacctg gggcaggctc taatttagtg gggctgggt tcaccctgaga
644461 ttctgtacta agtcctgtga tgatgtatc cttttttttttt cttttttttttt
644521 tagtaggtt taagaacattt cttttttttttt cttttttttttt
644581 ttactgctta ggaaaaatgg caataaaatc tttttttttttt
644641 ttgcacaaat ctgtttttttt tttttttttttt
644701 ctcabctgtga cttttttttt tttttttttttt
644761 ttggatgt aatataaaat tttttttttttt
644821 tatctcgca tttagaccaca gaaatgtca tttttttttttt
644881 gtttagcaata ataaactaa tagaaatgtt gttttttttttt
644941 agggtcgtga cttcacacctt ttatccatgtt gttttttttttt
645001 aaattccaa aataatctta aaggaaaaaa ttatccatgtt gttttttttttt
645061 cttttttcgg caaaatttcgg gacaaggaaat ttatccatgtt gttttttttttt
645121 aggttcccttgg tgacatattt aggcaacttg cttttttttttt
645181 caggcagctt ttctctttttttt
645241 gccaabtagga ttttttttttt
645301 tttttttttttt
645361 taaaccccca taaacatttt accggaaaaaa ttatccatgtt gttttttttttt
645421 ctggggaccc tttttttttttt
645481 tttttttttttt
645541 caaatggaaaaaa ttatccatgtt gttttttttttt
645601 atggggatcta aaacaggatca tttttttttttt
645661 tttttttttttt
645721 ataaaattttt ctccccatggaa atggggatca tttttttttttt
645781 ggtttttttttt
645841 tggccatgtt cttttttttttt
645901 tttagtcca tttttttttttt
645961 agttttagca agggactgtttt
646021 tgggtggccaa ttatccatgtt gttttttttttt
646081 tatgtacatgc actgttgcgtt gttttttttttt
646141 atgataccatgtt tttttttttttt
646201 tgcaaaaatgtt tttttttttttt
646261 gttatccccc agaattttttttt
646321 gaaggcttagc gttttttttttt
646381 tggggatatac atggggatggggaa ttatccatgtt gttttttttttt

FIGURE 11N

646441 aaaggtaat tgaagctgtg tagattatgt gtgatcccg tagattatgt
646501 tcccgaccc actgttagaa gtcctttt gacagagata atgtggaaac agagtggaaa
646561 gcacatgtc ttggcagcc ctacaactca ttcaactcaa cttacttcaaa cttacttca
646621 gcaggaaatgg aaaaatgtct tgccatgtca ctgaactgtc ttacactctt
646681 ocaacacatt taatgttagaa tagccatgtca cttacaactga ccgttgttgg aaaaaggaca
646741 tttccactat gaaaaactaa cgacgttcta gggttgttgcactt tggggaaaggaa ggttgttca
646801 dactgtttcc ctataaacc caacttgcac aaaaaataag gggaaactgtg tctgtct
646861 ttcaattttt atatatataat atatataat atatataat atatataat acacacac
646921 acacatataat atgttatat ttatataat gttatgtttt tttttttttt tttaaggtag aaaaattatgg
646981 gaactaatctt caatattttca aatataattt tttttttttt aatataatttg aatatattttt gttttttttt
647041 atcaabgggt ttctttctaa aaaaatgtata aaaaatgtata gaaaggaggctg aaatataattt gattaatcaa
647101 ttcatatgtttttt atgtgtcatatgc tttttgtttttt gatttttttttt gttttttttt gttttttttt
647161 gttttttttt gtttttgatbt tt
647221 tacatgggg gcctgtcaaa gcaaaacta aggactatgg ttatggccact aatttttttca
647281 cacaatatgt ctcatttttt cacattatct acacacacac atatgtatttt tatgtaaac
647341 tacaggcgat tt
647401 tcctatgtaaat gaaccaggact actgtgtcaat tgcgttt
647461 accagggttac tggtcaatctt ctt
647521 gttcacatgtctt ctcattttttccataacat atttttttttgc gtttttttttttttttttttttttttttttttttttt
647581 agctactcat tagttatgcg ttt
647641 catggaaatgtt ctgggttcat gtt
647701 tccccatgtact ctgggttttccat gtt
647761 accccatgtgt gtggaaatatttataatcttccat gtt
647821 taatggcaaa ataaatggggattt
647881 agggccctca aaatctcaaa tt
647941 acttttgttctt atteggattt taaaaggattt gtt
648001 tgtttctgtt gttttttagca ctt
648061 ctt
648121 ttccatccatca aatggggat ttt
648181 ttccacagggtt aatggggat ttt
648241 aaactaaat tt
648301 actgggttttttccacttggca aatggggat ttttttttttttttttttttttttttttttttttttt
648361 aaaaatgttcat gtt
648421 tatttttttttccacttgcat ttt
648481 ctggcccata gtt
648541 ctgttccaagc atagggaaaga gaaaccaggc ttttttttttttttttttttttttttttttttttttttt

1

**PHARMACOGENETIC TEST
ANTI-RESORPTIVE THERAPY-ASSOCIATED
OSTEONECROSIS OF THE JAW**

PRIORITY CLAIM

This application claims priority to U.S. Provisional Application Ser. No. 61/471,532, filed Apr. 4, 2011, the contents of which is incorporated by reference in its entirety herein.

SEQUENCE LISTING

The instant application contains a Sequence Listing which has been submitted in ASCII format via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Nov. 19, 2012, is named 07005045.txt and is 59,951 bytes in size.

GRANT INFORMATION

This invention was made with government support under Grant No. DE018143-01 awarded by the National Institute of Dental and Craniofacial Research, National Institutes of Health. The government has certain rights in the invention.

1. INTRODUCTION

The present invention relates to methods and compositions for determining whether a subject is at increased risk for developing anti-resorptive therapy-related osteonecrosis of the jaw.

2. BACKGROUND OF THE INVENTION

Bisphosphonates (BPs) are widely prescribed anti-osteoclastic medications. The intravenously administered BPs pamidronate and zoledronic acid are used in oncology to control bone metastasis and hypercalcemia. Oral BPs are used to control or prevent bone loss in osteoporosis, including osteoporosis associated with menopause. An estimated 3 million American women are currently being treated with oral bisphosphonates [1]. The monoclonal antibody Denosumab is also used to treat these conditions.

BPs are synthetic analogs of pyrophosphate that readily localize to bones due to their affinity for hydroxyapatite, and reduce osteoclastic activity. They are not readily metabolized, and thus, have long-lasting effects that might extend for several years. BPs are especially attracted to, and localize in, areas of the bone undergoing inflammation or resorption. They are subsequently phagocytized and internalized by osteoclasts. These internalized bisphosphonates, in turn, trigger apoptosis (cell death) of the osteoclasts, thus inhibiting osteoclast-mediated bone resorption [2]. Osteoclasts seem to be affected by BPs both in terms of number and function. Animal studies have also demonstrated some antiangiogenic properties, which may partially explain the development of osteonecrosis due to limited healing ability of the bone because of reduced vasculature [3].

BPs, especially zoledronic acid, have been associated with a serious adverse effect, osteonecrosis of the jaw. According to the American Association of Oral and Maxillofacial Surgeons (AAOMS), BP-related osteonecrosis of the jaw (BRONJ) is defined as exposed bone in the maxillofacial region for more than eight weeks in patients treated with a bisphosphonate that have no prior history of radiation therapy to the jaws [4]. The non-healing exposed necrotic lesions may involve the mandible or the maxilla or both, and can be

2

painful, persistent, and resistant to treatment. The incidence of BRONJ varies in different studies. BRONJ affects as many as 5-10% of zoledronic acid users and far fewer users of oral bisphosphonates.

- 5 Osteonecrosis of the jaw has also been reported in association with denosumab treatment [29]. It would be desirable to identify individuals who are at risk for developing osteonecrosis of the jaw, so that subjects at greater risk could be considered for alternatives to anti-resorptive therapy or, if 10 suitable alternatives are not available, could be monitored more closely.

3. SUMMARY OF THE INVENTION

- 15 The present invention relates to methods and compositions for testing individuals to determine whether they are at increased risk of developing anti-resorptive therapy-associated osteonecrosis of the jaw ("ARONJ"). It is based, at least in part, on the results of a genome wide association analysis 20 which revealed that certain Single Nucleotide Polymorphisms ("SNPs") are significantly associated with osteonecrosis of the jaw among bisphosphonate users, including SNPs in the RNA-binding motif, single-stranded-interacting protein 3 ("RBMS3") gene (for example, the SNP rs17024608) as well as SNPs in other genes, including but not limited to those for insulin-like growth factor I receptor ("IGF1R"), insulin-like growth factor binding protein 7 ("IGFBP7"), dihydropyrimidine dehydrogenase ("DPYD"), ATP-binding cassette, sub-family C (CFTR/MRP), member 4 ("ABCC4"), and glutathione S-transferase mu 2 ("GSTM2") and other SNPs as listed in TABLES 1-5.

4. BRIEF DESCRIPTION OF THE FIGURES

- 35 The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawing(s) will be provided by the Office upon request and payment of the necessary fee.

40 FIG. 1A-B: Population structure of Caucasian subjects from the combined ONJ/Hap Map 3/European collections. The red circles represent ONJ subjects, azure dots CEU Hap Map 3, blue dots CEU Hap Map III, yellow dots North European POPRES, green dots central European POPRES, gray dots Spanish POPRES, light yellow dots South European POPRES. (A) PC axis 2 versus PC axis 1 (ordinate versus abscissa). (B) PC axis 1 versus PC axis 3 (ordinate versus abscissa).

45 FIG. 2. QQ plot for Caucasian ONJ Study Group.

FIG. 3. Manhattan Plot for Caucasian ONJ Study Group.

- 50 FIG. 4: Manhattan Plot of the region surrounding rs17024608. Red dots represent the imputed markers; Gray dots represent the original markers.

55 FIG. 5A-B. Results of SNP analysis within 20 kb of IGF gene family candidate genes. (A) QQ for candidate SNPs (logistic test, drug-exposed study group) and (B) SNP quality graph of the top hit.

60 FIG. 6A-B. Results of SNP analysis of ADME genes. (A) QQ for ADME SNPs (logistic test, drug-exposed study group) and (B) SNP quality graph of the top hit.

65 FIG. 7A-B. SNP analysis of IGF-related SNPs in the extended study group. (A) QQ plot for candidate SNPs (logistic test, extended study group) and (B) SNP quality graph of the top hit.

65 FIG. 8A-B. SNP analysis of ADME-related SNPs in the extended study group. (A) QQ plot for ADME SNPs (logistic test, extended study group) and (B) SNP quality graph of the top hit.

FIG. 9. QQ plots for IGF-candidate SNPs (logistic test, final study group).

FIG. 10A-B. (A) QQ plots for ADME SNPs (logistic test, final study group) and (B) SNP quality graph of the top hit.

FIG. 11A-Q. Nucleotide sequence (SEQ ID NO: 86) of the intron between positions 29941247 to 29977576 of the human RBMS3 gene on chromosome 3 (numbered consistently with their the numbering of the RBMS3 gene as represented in NCBI Ace. No. NC_000003 Region 29322803 . . . 30051886 GPC_000000027). Sequence flanking the A/G substitution in rs17024608 is bolded and underlined, and the variant base (A) involved in the A to G substitution is shown by a capital letter. For clarity, residue 618421 in the figure is residue 29941247 of human chromosome 3.

5. DETAILED DESCRIPTION OF THE INVENTION

For purposes of clarity of description and not by way of limitation, the detailed description of the invention is divided into the following subsections:

- (i) biomarker genes and SNPs;
- (ii) methods of treatment/diagnosis; and
- (iii) kits.

The term “anti-resorptive therapy” as used herein refers to therapy in which an agent (“anti-resorptive agent”) is administered that inhibits resorption of bone, for example in the treatment of osteoporosis or in oncology to control bone metastasis and/or hypercalcemia. Non-limiting examples of anti-resorptive agents include, but are not limited to, bisphosphonates and monoclonal antibodies specific for RANK ligand, such as, but not limited to, denosumab.

“Anti-resorptive therapy-associated osteonecrosis of the jaw”, or “ARONJ”, includes BRONJ as well as ONJ associated with other anti-resorptive agents.

The term “bisphosphonates” as used herein refers to a class of drugs comprising a bisphosphonate structure that may be used to treat osteoporosis or hypercalcemia. Non-limiting examples of bisphosphonates include orally-administered drugs such as alendronate (Fosamax), etidronate (Didronel), ibadronate (Boniva), and risedronate (Actonel) and intravenously administered drugs such as pamidronate (Aredia) and zoledronic acid (Zometa).

The term “osteonecrosis of the jaw” (“ONJ”) means a clinical condition characterized by, in a subject, exposed bone in the maxillofacial region that persists for more than eight weeks. Typically one or more region of the affected bone area is necrotic.

The term “allelic variation” refers to the presence, in a population, of different forms of the same gene characterized by differences in their nucleotide sequences (sequences in genomic DNA). The variation may be in the form of one or more substitution, insertion, or deletion of a nucleotide. Different alleles may be functionally the same, or may be functionally different. In one subset of allelic variations a single nucleotide is different between alleles, and is referred to as a Single Nucleotide Polymorphism (“SNP”). Allelic variation in a known sequence may be identified by standard sequencing techniques. A “variation” or “variant,” as those terms are used herein, is relative to the ancestral gene found in the majority of the population. Unless specified otherwise, the presence of a SNP means that at the single nucleotide position for which alleles have been identified, the nucleotide present is the variant nucleotide, not the nucleotide found in the majority of the population (however, TABLE 4 lists SNPs and then specifies which allele is associated with ARONJ, and either the allele found in the majority of the population or a

variant may be specified). The variation (variant) is comprised of a substituted nucleotide or nucleotides or an insertion or deletion of a nucleotide or nucleotides. Herein, generally the ancestral nucleotide is listed first and the variation (variant) nucleotide is listed second (for example, in A/G A is the ancestral nucleotide and G is the variation (variant) nucleotide). If there is an insertion, the ancestral nucleotide is represented by a hyphen (e.g., -/G). If there is a deletion, the variation (variant) nucleotide is represented by a hyphen (e.g., G/-). Numerous allelic variations (variants), captured in SNPs, of gene s are known in the art and catalogued (for example, in the National Center for Biotechnology Information “Entrez SNP”). Allelic variations that are not SNPs include deletions or insertions or substitutions of multiple consecutive nucleotides.

In non-limiting embodiments of the invention, the presence of an allelic variation, for example a SNP, may be determined using a technique such as, but not limited to, primer extension or polymerase chain reaction, using primer(s) designed based on sequence in the proximity of the variation, followed by sequencing. For example, and not by way of limitation, the presence of a SNP indicative of increased risk of ARONJ may be determined by a method comprising using at least one primer sequence complementary to a sequence flanking the location of the SNP (for example, within 80 nucleotides, or within 50 nucleotides, or within 30 nucleotides, or within 20 nucleotides, or within 10 nucleotides, of the SNP) in a primer extension reaction or polymerase chain reaction to generate a test fragment that contains the location of the SNP and determining the nucleotide present at the location of the single nucleotide polymorphism, for example by sequencing all or a portion of the test fragment.

A subject may be a human or a non-human subject. In a specific non-limiting embodiment, the subject suffers from osteoporosis. In a specific non-limiting embodiment, the subject is a postmenopausal woman. In a specific non-limiting embodiment, the subject has a cancer and has or is at risk for bone metastasis. In a specific non-limiting embodiment the subject has hypercalcemia.

To assess whether the subject carries a ARONJ biomarker as described herein, a sample of nucleic acid from the subject may be used. The nucleic acid may be genomic DNA or RNA reflective of the allelic variation or a cDNA copy thereof. For example, a sample comprising a cell from the subject may be collected. For example, the sample may be a tissue or body fluid, including but not limited to saliva, blood or its components, skin, hair follicle, urine, etc. The sample may be obtained by scraping the inside of the subject’s mouth or cervix (eg in the context of a Pap smear). In a non-limiting example, as part of the detection process, nucleic acid may be at least partially purified from the sample.

5.1 Biomarker Genes and SNPs

In various non-limiting embodiments, the following genes and SNPs have been related to ARONJ, such that these genes and SNPs may be used as biomarkers for increased risk of ARONJ. Allelic variation and SNP variants may be used as indicators that a subject is at increased risk for ARONJ. The genes listed below, SNPs associated with those genes, and the further SNPs listed below are collectively referred to herein as “ARONJ biomarkers”.

5.1.1 RBMS3

RBMS3 is an RNA-binding protein that belongs to the c-myc gene single-strand binding protein family. Its tran-

5

scripts are alternatively spliced to form different mRNAs. In humans it is located at about positions 29322803-30051886 on chromosome 3 (NCBI Reference Sequence NC_00003.11).

In one non-limiting embodiment of the present invention, an allelic variation in the RBMS3 gene, where the allelic variation may be a SNP, is an indicator that a subject is at increased risk for developing ARONJ.

In another non-limiting embodiment of the present invention, an allelic variation in a region of RBMS3 from about positions 29900000 to 29990000 of the human gene on chromosome 3 (see NC_00003.11), where the allelic variation may be a SNP, is an indicator that a subject is at increased risk for developing ARONJ.

In another non-limiting embodiment of the present invention, an allelic variation in the intron of RBMS3 from about positions 29941247 to 29977576 of the human gene on chro-

6

mosome 3, where the allelic variation may be a SNP, is an indicator that a subject is at increased risk for developing ARONJ. The sequence of this intron is set forth in FIG. 11.

In another non-limiting embodiment of the present invention, an allelic variation in a region of the intron of RBMS3 from about positions 29941247 to 29977576 of the human gene on chromosome 3, said region being between about 29954000 to 29955000 (between about nucleotides numbered 631198 and 632198 in FIG. 11), where the allelic variation may be a SNP, is an indicator that a subject is at increased risk for developing ARONJ.

In another non-limiting embodiment of the present invention, an allelic variant which is a SNP of RBMS3 selected from those set forth in TABLE 1 is an indicator that a subject is at increased risk for developing ARONJ. For clarity, the SNP is shown in bold text and underlined; for example, in rs17024608 the SNP is a substitution of ancestral nucleotide A by G, as shown by “A/G”.

TABLE 1

SEQ	SNP	
ID	ref	Chr 3
No.	no.	position Variation (bold, underlined)
1	rs17024608	29954690 GATAGAATAGAA <u>ACTATTGATGTGG<u>A/GCCATGAG</u></u> AATTAAA <u>AGTATCTGCA</u>
2	rs3821577	29910544 AAGGCAGACGTATGGGCCATGAT <u>GAA<u>/GATTGGTCCC<u>A</u></u> TGGAACACCCAA<u>TG</u></u>
3	rs9820707	29954837 TGAGAA <u>ATGACAGAAAA<u>ACTATAT<u>CAT<u>/CCAGCAGAGAA<u>AACATCTTCTGCTG</u></u></u></u></u>
4	rs9875937	29954551 ATTGAGGGCAGGCATAAGAC <u>CT<u>CTTG<u>/TCTATCATCA<u>CT</u></u></u> AGGTGGCT<u>CATAAA</u></u>
5	rs9876178	29954887 TGACCTAGGA <u>AGGCATACAA<u>ATAG<u>TTC<u>/AAGTTGGCGTCA<u>C<u>ACTGTTATGCAT</u></u></u></u></u></u>
6	rs13319154	29954187 ACTTCA <u>ATTTCT<u>GAAGAA<u>ATGT<u>T<u>/GGGCA<u>ACTACAT<u>TAATATTCTCAG</u></u></u></u></u></u></u>
7	rs13326291	29954399 CTCATGGAAA <u>AGATGG<u>CAAG<u>ATTG<u>TT<u>/CAGTTGTGCC<u>GA<u>ATTTCT<u>TAAT</u></u></u></u></u></u></u></u>
8	rs75830538	29954957 GTGGTACTTGTCC <u>CTTT<u>TATAT<u>CACT<u>/CTAACATA<u>AGTAT<u>A<u>ATTCATTGCAC</u></u></u></u></u></u></u>
9	rs114730671	29954785 TCTATCTACA <u>ATA<u>ATT<u>ACT<u>CAAT<u>AT<u>G<u>/TTTCAGCAG<u>ACTC<u>TGAA<u>ATCTGC<u>ACT</u></u></u></u></u></u></u></u></u></u></u>
10	rs116600197	29954066 TCAGCTGAA <u>ACA<u>ACTG<u>TGTT<u>T<u>ATC<u>AGC<u>/TGTAGTGT<u>CTTAA<u>TTGGCAGTT<u>ACAT</u></u></u></u></u></u></u></u></u></u>
11	rs116863073	29954716 ACCATGAGA <u>ATT<u>AAA<u>AGT<u>TAT<u>CTGC<u>AT<u>/CAA<u>ATTG<u>ATG<u>GAT<u>TTGGC<u>CAT<u>CA<u>GA<u>TAA</u></u></u></u></u></u></u></u></u></u></u></u></u></u></u>
12	rs118013282	29954445 CTTAATA <u>AA<u>ATG<u>TCT<u>CAA<u>AGC<u>CT<u>TC<u>CAC<u>/TAGGAG<u>CCCC<u>AA<u>G<u>CAT<u>TG<u>TAC<u>ACAG<u>TTG</u></u></u></u></u></u></u></u></u></u></u></u></u></u></u></u></u>

In another non-limiting embodiment of the present invention, an allelic variant which is a SNP of RBMS3 as occurs in rs17024608, shown in TABLE 1, is an indicator that a subject is at increased risk for developing ARONJ.

In another non-limiting embodiment of the present invention, an allelic variant which is a substitution of A by G at position 29954690 of chromosome 3 is an indicator that a subject is at increased risk for developing ARONJ.

In another non-limiting embodiment of the present invention, an allelic variant which is a substitution of A by G in SEQ ID NO: 1: (GATAGAATAGAACTATTGATGTGG A/GCCATGAGAATTAAAAGTATCTGCA) at the position indicated by A/G, is an indicator that a subject is at increased risk for developing ARONJ.

In another non-limiting embodiment of the present invention, an allelic variant which is a SNP of RBMS3 selected from those set forth in TABLE 2 is an indicator that a subject is at increased risk for developing ARONJ.

mosome 4 (see NC_000004.11), where the allelic variation may be a SNP, is an indicator that a subject is at increased risk for developing ARONJ.

In another non-limiting embodiment of the present invention, an allelic variation in a region of IGFBP7 from about positions 57940000 to 57950000 of the human gene on chromosome 4 (see NC_000004.11), where the allelic variation may be a SNP, is an indicator that a subject is at increased risk for developing ARONJ.

In another non-limiting embodiment of the present invention, an allelic variation which is a SNP of IGFBP7 as occurs in rs11934877 is an indicator that a subject is at increased risk for developing ARONJ. The SNP of rs11934877 is located at position 57941026 of chromosome 4, where the ancestral nucleotide T is replaced by C, for example as in SEQ ID NO:15

TABLE 2

SEQ ID NO.	SNP ref no.	Chr 3 position	Variation
13	rs10510628	29853403	GCTCTGCCGTTCTTAGGAAGTTGTGG/ <u>AAAGATATTGGT</u> CTTTTGTAAT
14	rs4599260	29853269	CCATTAGATAAA <u>GAT</u> / <u>CGAGTGACCTCA</u> AAAAA
15	rs10514681	29853882	TAGTGGAAAGTTAAAGAGACCGTC/ <u>TATTGAGTGCTT</u> TGATATGTTGTTC
16	rs35393422	29853420	GAAGTTGTGGAAAGATATTGGTCTTTT/- GTGAATATGTATGACACTATTATT
17	rs79049188	29853041	CTCTCATGGAGTCTACATTCTAAGGTC/ <u>TTCATAGGAAAC</u> ACATGTAACATTAC
18	rs115136555	29853407	TGCCGTTCTTAGGAAGTTGTGGAA <u>G</u> /GTATTGGTCTTT TGTGAATATGTAT

5.1.2 IGF1R

The IGF1R gene in humans is located at about positions 99145510 to 99555008 on chromosome 15 (NCBI Reference Sequence NG_009492).

In one non-limiting embodiment of the present invention, an allelic variation in the IGF1R gene, where the allelic variation may be a SNP, is an indicator that a subject is at increased risk for developing ARONJ.

5.1.3 IGFBP7

The IGFBP7 gene in humans is located at about positions 57897244 to 57976539 on chromosome 4 (NCBI Reference Sequence NC_000004.11).

In one non-limiting embodiment of the present invention, an allelic variation in the IGFBP7 gene, where the allelic variation may be a SNP, is an indicator that a subject is at increased risk for developing ARONJ.

In another non-limiting embodiment of the present invention, an allelic variation in a region of IGFBP7 from about positions 57920000 to 57950000 of the human gene on chromosome 4 (see NC_000004.11), where the allelic variation may be a SNP, is an indicator that a subject is at increased risk for developing ARONJ.

In another non-limiting embodiment of the present invention, an allelic variation in a region of IGFBP7 from about positions 57930000 to 57940000 of the human gene on chro-

40 TAATCTGTGTTAAACAATATAGCATT/CATCTGCTTGATGCACTA
GGCACC.

In another non-limiting embodiment of the present invention, an allelic variation which is a SNP of IGFBP7 as occurs in rs17761305 is an indicator that a subject is at increased risk for developing ARONJ. The SNP of rs17761305 is located at position 57934091 of chromosome 4, where the ancestral nucleotide C is replaced by T, for example as in SEQ ID NO 50 20:

CCCCCTGGAGAATAATTGATAGGGTAGC/TGAAAAATGTGGATATCATA
AAATAT.

5.1.4 DPYD

The DPYD gene in humans is located at about positions 60 (-)98513111 to (-)97416801 on the negative strand of chromosome 1 (NCBI Reference Sequence NG_008807.1)

In one non-limiting embodiment of the present invention, an allelic variation in the DPYD gene, where the allelic variation may be a SNP, is an indicator that a subject is at increased risk for developing ARONJ.

In another non-limiting embodiment of the present invention, an allelic variation in a region of DPYD gene from about

9

positions (-)97800000 to (-)97500000 of the human gene on chromosome 1 (see NG_008807.1), where the allelic variation may be a SNP, is an indicator that a subject is at increased risk for developing ARONJ.

In another non-limiting embodiment of the present invention, an allelic variation in a region of DPYD gene from about positions (-)97700000 to (-)97650000 of the human gene on chromosome 1 (see NG_008807.1), where the allelic variation may be a SNP, is an indicator that a subject is at increased risk for developing ARONJ.

In another non-limiting embodiment of the present invention, an allelic variation which is a SNP of DPYD as occurs in rs10875055 is an indicator that a subject is at increased risk for developing ARONJ. The SNP of rs10875055 is located at position (-)97683997 of chromosome 1, where the ancestral nucleotide C is replaced by T, for example as in SEQ ID NO:21:

TTCATCTCACTAATAAGAGCTACCCAC/TCCGCCTTATACAGAGGTT
CTCAGA

5.1.5 ABCC4

The ABCC4 gene in humans is located at about positions 95672083-95953687 on chromosome 13 (NCBI Reference Sequence NC_000013.10).

In one non-limiting embodiment of the present invention, an allelic variation in the ABCC4 gene, where the allelic variation may be a SNP, is an indicator that a subject is at increased risk for developing ARONJ.

In another non-limiting embodiment of the present invention, an allelic variation in a region of ABCC4 gene from about positions 95730000 to 95740000 of the human gene on chromosome 13 (see NC_000013.10), where the allelic variation may be a SNP, is an indicator that a subject is at increased risk for developing ARONJ.

In another non-limiting embodiment of the present invention, an allelic variation in a region of ABCC4 gene from about positions 95732000 to 95738000 of the human gene on chromosome 13 (see NC_000013.10), where the allelic variation may be a SNP, is an indicator that a subject is at increased risk for developing ARONJ.

In another non-limiting embodiment of the present invention, an allelic variation which is a SNP of ABCC4 as occurs

10

in rs1189437 is an indicator that a subject is at increased risk for developing ARONJ. The SNP of rs1189437 is located at position 95735604 of chromosome 13, where the ancestral nucleotide A is replaced by C, for example as in SEQ ID

5 NO:22:

GAGTGTAATCCTAACAAACTCATGA/CAAGTATTTTGAAAAGAA
TACTTGA.

5.1.6 GSTM2

The GSTM2 gene in humans is located at about positions 110210644 to 110226619 on chromosome 1 (NCBI Reference Sequence NC_000001.10).

In one non-limiting embodiment of the present invention, an allelic variation in the GSTM2 gene, where the allelic variation may be a SNP, is an indicator that a subject is at increased risk for developing ARONJ.

In another non-limiting embodiment of the present invention, an allelic variation in a region of GSTM2 gene from about positions 110210000 to 110215000 of the human gene on chromosome 3 (see NC_000001.10), where the allelic variation may be a SNP, is an indicator that a subject is at increased risk for developing ARONJ.

In another non-limiting embodiment of the present invention, an allelic variation which is a SNP of GSTM2 as occurs in rs673151 is an indicator that a subject is at increased risk for developing ARONJ. The SNP of rs673151 is located at position 110213458 of chromosome 1, where the ancestral nucleotide G is replaced by A, for example as in SEQ ID NO:23:

GAAAGATGAGGAGATATTAGAGGATG/AAGTGGAGAAAGGAGGG
GGAAAAAG.

5.1.7 Further SNP Biomarkers

In further non-limiting embodiments of the present invention, the presence of an allelic variation which is a SNP selected from those set forth in TABLE 3 is an indicator that a subject is at increased risk for developing ARONJ.

TABLE 3

SEQ	SNP	Chromosome	
ID	ref	location/	Variation
NO.	no.	gene	
24	rs8012823	72343297chr14	CTGGAGGGCTCCAAT/ <u>CGGACTGATCTCTTG</u> DPF3 gene
25	rs11802277	Chr. 1	GAGAGTGAGAACTGAGTGGGCTGGGGAGCT <u>G/TATGGACTTACCTGCCATTCTAACCC</u>
26	rs10754178	196416252chr 1	TTCTTTCCATCTCAA/ <u>GTGAAATATTTGCCT</u> KCNT2
27	rs13096022	7425350 chr3	TCAGGA/ <u>GTAAAC</u> GRM7
28	rs6900513	66333105chr6	GATAACCTCCAAAGAC/ <u>TTTGGTTGTAATTTC</u> EYS
29	rs1873291	66344855chr6	TTAAAAATCAATTGC/ <u>TCTTCATCACAGACAG</u> EYS

TABLE 3-continued

SEQ NO.	SNP ID	Chromosome location/ gene	Variation
30	rs10781262	77650696chr9	TTAATAAAGGGTAAGATTGGGCTAT <u>C</u> /GTATTGAATT AGCAGAACACTCTA
31	rs1471646	chr 1 RP11-382E9.1	GACTCATCTGACTTAGAAATGGGTGG[A/G]TGAAAAG <u>A</u> ATCTTCACTCACTATGT
32	rs4870310	chr 6 RP11-15G8.1	ancestral gene nucleotide is T; variant is C CTCGTTGTTTCTGGCACTACAAGAT/CGTCCAGGTC ATCTTATATATTCT
33	rs10875148	98859508chr1	ancestral gene nucleotide is G; variant is A TATTTCTAACTCTTCTGGTATAAT <u>G</u> /AGAACAGTC GATCTGAACAAAGAG
34	rs4562759	83835639chr10 NRG3	ancestral gene nucleotide is T; variant is C AGAGAGTAGAATTAAAGTGGTTTC <u>A</u> /CTGGAATTATG GAGGGAGAATGAAT
35	rs4878512	27630418chr9 RP11-53518.1	ancestral gene nucleotide is A; variant is G AAGAATGTAAGCATTCTACTGCT <u>A</u> /GTTCCCTTC TGTTTGTTTCTCT
36	rs12613966	AC113618.1	ancestral gene nucleotide is C; variant is T AAATGTCACCTTGAGTAGTGAAG <u>TTC</u> /TTGGATGATT TATTTCTTATTT
37	rs11189381	RP11-459F3.3	ancestral gene nucleotide is T, variant is C GCTGGCTTCTCTTAATCAGAACTG <u>C</u> /CCTTAGCTCAA GAGAGGCTGGAAA
38	rs6861122	AC022120.1	ancestral gene nucleotide is C; variant is T TTAGTAATATGCCTTAAGGTAC <u>CTCC</u> /TATCTAAACTGA ACATGCTCATTA
39	rs4431170	MARCH1	ancestral gene nucleotide is A; variant is G TGAAACCAA <u>A</u> TAAACTACTCT <u>A</u> /GTCTTGTGAGA GAATTCCAGGGCAC

In another non-limiting embodiment of the present invention, an allelic variant which is a SNP of the human EYS gene in a region on chromosome 6 between 66325000 and 66350000, where the allelic variation may be a SNP, is an indicator that a subject is at increased risk for developing ARONJ.

In further non-limiting embodiments of the present invention, an allelic variation which is a SNP selected from those set forth in TABLE 4 is an indicator that a subject is at increased risk for developing ARONJ, where the nucleotide in the column marked "allele" is the allele indicative of the increased risk (among the SNPs listed in TABLE 4, some-

times the allele associated with ARONJ is the variant allele, and sometimes it is the allele found in the majority of the population tested). The SNPs listed in TABLE 4, except for rs17024608 which is discussed above, are denoted SNP ID #40-147. Commercial probes or sequences corresponding to the SNPs listed in TABLE 4 are publicly available, either for the SNP named (e.g., "rs17024608") or at the chromosomal position specified (e.g., "12-85466404" denotes a SNP found at position 85466404 on human chromosome 12). For convenience, and not by way of limitation, the sequences of certain regions containing SNPs are set forth in TABLE 5 below as SEQ ID NOS: 40-85.

TABLE 4

CHR	SNP	LOCATION	ALLELE	TESTED	SAIOR	SE	L95	U95	STAT	P. value	SNP ID#
3	rs17024608	29954690	G	1744	5.825	0.3276	3.065	11.07	5.379	7.47E-08	
22	rs5768434	46977516	T	1752	12.61	0.4784	4.937	32.2	5.298	1.17E-07	40
12	rs11064477	6944626	A	1689	21.66	0.6126	6.52	71.98	5.02	5.16E-07	41
12	12-85466404	85466404	A	1696	9.296	0.4769	3.65	23.67	4.675	2.95E-06	42
8	8-58133986	58133986	T	1746	7.326	0.427	3.173	16.92	4.664	3.10E-06	43
1	rs1886629	194421521	C	1755	3.698	0.2878	2.104	6.501	4.544	5.53E-06	44
2	rs7588295	166115757	G	1716	8.681	0.4783	3.399	22.17	4.518	6.24E-06	45
4	rs4431170	165504024	G	1748	5.176	0.3665	2.523	10.62	4.485	7.28E-06	46
6	rs7740004	120897902	A	1757	5.952	0.3992	2.722	13.02	4.469	7.87E-06	47
10	rs11189381	99553188	C	1728	6.816	0.4303	2.933	15.84	4.461	8.17E-06	48
15	rs12903202	56094085	G	1690	4.036	0.3145	2.179	7.477	4.436	9.15E-06	49
18	rs17751934	47455812	T	1773	5.009	0.3632	2.458	10.21	4.436	9.16E-06	50
11	11-23990403	23990403	C	1708	12.17	0.5655	4.016	36.86	4.419	9.94E-06	51
3	rs7613687	60124976	T	1733	13.44	0.6107	4.061	44.49	4.255	2.09E-05	52
3	rs7634338	8864809	C	1708	12.55	0.6001	3.87	40.68	4.215	2.50E-05	53
3	rs7612449	181586884	T	1718	11.79	0.5708	3.853	36.1	4.323	1.54E-05	54

TABLE 4-continued

CHR	SNP	LOCATION	ALLELE	TESTED	SA OR	SE	L95	U95	STAT	P. value	SNP ID#
14	rs12431810	98044037	A	1744	7.33	0.4777	2.874	18.7	4.17	3.05E-05	133
8	8-91414191	91414191	A	1707	7.312	0.4836	2.834	18.86	4.114	3.88E-05	134
2	rs312047	21328107	A	1686	7.236	0.4866	2.788	18.78	4.067	4.76E-05	135
20	rs2297429	61699516	T	1726	7.208	0.506	2.673	19.43	3.903	9.49E-05	136
3	3-29883350	29883350	A	1751	7.182	0.4669	2.876	17.93	4.222	2.42E-05	137
2	2-81311658	81311658	C	1750	7.18	0.4836	2.783	18.52	4.077	4.57E-05	138
3	rs12638932	29882677	T	1749	7.171	0.4669	2.872	17.91	4.219	2.45E-05	139
3	3-29881826	29881826	C	1748	7.166	0.4669	2.87	17.89	4.218	2.47E-05	140
2	rs1986414	201199695	A	1711	7.164	0.4573	2.924	17.56	4.306	1.66E-05	141
3	3-29884382	29884382	C	1758	7.126	0.4674	2.851	17.81	4.202	2.65E-05	142
2	rs2219366	81318138	A	1748	7.118	0.4834	2.76	18.36	4.06	4.90E-05	143
19	19-55069295	55069295	C	1732	7.111	0.5022	2.658	19.03	3.906	9.37E-05	144
9	9-17634306	17634306	T	1755	7.102	0.5027	2.651	19.02	3.9	9.63E-05	145
10	rs1886951	2425384	A	1686	7.085	0.456	2.899	17.32	4.294	1.75E-05	146
19	19-55072907	55072907	T	1735	7.054	0.502	2.637	18.87	3.892	9.95E-05	147

TABLE 5

CHR	SNP	LOCATION	AL- LELE	SNP ID ID# NO:	SEQ Sequence						
					SEQ	AL- LELE	SNP ID ID# NO:	Sequence	SEQ	AL- LELE	SNP ID ID# NO:
22	rs5768434	46977516	T	40 40	TTTGTATCTAATGTTATATTcttta	[C/T]	gcttgaactatggcattcta				
12	rs11064477	6944626	A	41 41	AGCCTTCCCAGCTGGTCCTGTTTC	[A/G]	GAGCCAGGCCTGCTTCCCCTAG				
1	rs1886629	194421521	C	44 42	GAATCTCCAAGTTAATTTTCATTG	[C/T]	TTACCTTTTAACTGCATGAAGTC				
2	rs7588295	166115757	G	45 43	ACTTTTTTTCAATTCTGAAATCA	[A/G]	CTTCTTAGATCTACTTTCCCTTACC				
4	rs4431170	165504024	G	46 44	TGAAACCAAATATAAACACTTCTT	[A/G]	TCTTTGTGAGAGAATTCCAGGGCAC				
6	rs7740004	120897902	A	47 45	TACAACCTCTCAAGAAGCAATTTTT	[A/T]	TGGCAGGAAGCTGCATGAGTGATAA				
10	rs11189381	99553188	C	48 46	GCTGGCTCTCTTAATCAGAACTGC	[C/T]	CTTAGCTCAAGAGAGGCTGGAAAA				
15	rs12903202	56094085	G	49 47	CACTGATGCTAAGGCAAGAGTTATCG	[A/G]	TAGCCCAAGCTCTGGCTAGTATCCA				
18	rs17751934	47455812	T	50 48	ATAGAATAAATAAGGTAACAGGTAAT	[C/T]	AAACAAAGAGAAAAATATCTATT				
3	rs7613687	60124976	T	52 49	GGGAAATGAATCCCTGGCAGGATGGA	[C/T]	ATTAACCAACACCTAACACATCAG				
3	rs7634338	8864809	C	53 50	GGGAATATATGGTATTAAATGAAAGCA	[C/T]	TGCTCACACCTAGGTACCCCATACCT				
3	rs7612449	181586884	T	54 51	TTAAGTTATTGCTATCCTATCCTTCT	[C/T]	CAAAGAGCTTCTCTGTTTTTA				
4	rs10029016	8496903	A	55 52	gtggaaaggatggttaccagagggtgg	[A/G]	aaggggagtggagggtggggaga				
12	rs10505722	1102632	G	56 53	AATGATAAGCTTAAGAAAATACAAGC	[A/C/G/T]	TAAGTATGGCTCTTAATACGCTAGA				
14	rs2332834	71952831	C	57 54	GTCTCCTTTCTCTGTCCCCGT	[C/T]	TCAGCTCTGAATGAGAAAAGTTTG				
7	rs10271074	78589212	G	58 55	TATAAAGTCATCCTACTTCTCTTC	[A/G]	TACTTCAAAAGTTGGTATTCACTA				
1	rs4951362	202580842	C	61 56	GGCGAGAAAAGACATATGTGGATGGA	[C/T]	ATTCAGAACAACTTGTATTCCAA				
2	rs62153910	96382119	T	62 57	CTACACTGGGGTCCCAGAAGAGCTG	[C/T]	CCCCCTCTGCACATTCCAATGCAG				
15	rs7176436	56752223	G	68 58	TTATGAAAAGGCTGTGAAGCTGAAGA	[A/G]	AAACTAAGAAATGGATATTGCTGCA				
1	rs17127107	65099496	G	70 59	GTGGTTCATCTCATAGCAGACTGCT	[C/G]	AGAGGTGAAACTCCGGATTTA				
2	rs62156621	79426168	A	72 60	CACTCACACTGTGCCAGAGTTCTCCT	[A/T]	TGCTTCTACTCTTCTGAAATCCT				
2	rs921245	137980811	C	73 61	TAGCTCCACAAACATTCCCAGGCTAC	[A/G]	AGAGCTTACAGTCCATTAGCACTGA				
1	rs1736563	169371174	A	77 62	TTAAATCACAAATGCAGTCTCAATCC	[A/G]	GAAAATAGATCCCATCATATGTGAT				
12	rs4639998	85442168	T	85 63	tctttctcatatgtgttcctt	[C/T]	aggagctctagtaaggcaggctgg				
4	rs7669796	160863851	G	86 64	gc当地gggtgcctgcaggccatgc	[G/T]	gagccacccctcagaccccttcgc				
12	rs17653326	85528244	A	87 65	AGGAGGATATATAACCCCTGGCTGAA	[A/G]	AAGATGGAGATAGCTACAAGAGATG				
9	rs17057133	73509497	C	88 66	GTTGGACGGATACTCATCTCGTGTAA	[C/T]	GGTCATAGAAAGATTCTGAGTGCTC				

TABLE 5-continued

CHR SNP	LOCATION	AL-LELE	SNP ID	SEQ NO:	Sequence
16 rs3135009	12556820	T	89 67	CTCATGTACGCAGGGTGTTCCTAG[C/T]TGACATGCTGAGGACGTCTTCGT	
2 rs2544530	15820699	G	91 68	TTCCAAACCCGGCTTCCTCATTG[A/G]TCCTCAAACACCCATCGGGGGGCC	
8 rs16915413	94070482	A	92 69	TAGCCATTGACAAACCTGTAGACAT[A/G]AGAATTAAATATGTGATAAAAGATAA	
16 rs2856790	12557384	C	98 70	CACTTGTCCGTGGACTCATGCCATG[C/T]CACCGTAGTGCTGAGTGACGCTTAA	
3 rs6443519	179112920	A	102 71	ttagtgcataaaactctgaataaact[A/C]gggtttgatggatgtatctaaaa	
2 rs7568908	79462538	T	106 72	TAGCAATGCAAGCATGTTGCCTTC[G/T]ATAGCTAAATGACTGCgtgattgct	
2 rs57446887	21316772	C	120 73	TTATTCCATGCTTGGCTGCATG[C/T]ATGTCTCTTTGAAAAGTGTATCT	
2 rs10203465	81260623	C	121 74	tggtaataattacaagaaaaatgtct[G/C]tacatgttcagtataaatgcacac	
1 rs2805873	57713578	A	125 75	TGGCTCCTGGGTGCAACATCCGGAC[C/T]GATGTCTTTATTGTTATTGtt	
7 rs11982678	54625449	A	128 76	tatacacacacatataATTAATGCTA[A/G]AAGGCTATACACAGAACACTATTG	
2 rs7602629	21323199	A	130 77	gaggcctcaggaagctttactgtatg[A/G]ctgtaggcaagttagagcaggcac	
3 rs12636997	29874808	G	132 78	AAAAAAATTCATCTTATATGTAGTAC[A/G]TAGTAATCTATAATATAAAATACA	
14 rs12431810	98044037	A	133 79	ATGTTGAGATAGTAGCACAGGAGGCC[A/C]GGGATTATTGGGTTATACACAGA	
2 rs312047	21328107	A	135 80	AAGAGAGAATCAAAGGCAGGTCTC[A/G]CAGCAGGCCTGGACATCTGTATC	
20 rs2297429	61699516	T	136 81	ACAAGAAAGCAAGAGCTGCCAGGGCC[C/T]CTTCCAGCAGGGAGGCTGACCCCTGC	
3 rs12638932	29882677	T	139 82	AAGCTCTGactgttaagggtgatgg[A/T]tatgttcattatcttgacaaatggtg	
2 rs1986414	201199695	A	141 83	CCTGTGCAAATGAAATGCTCATCCCC[A/G]CAAAGAAGGAATATGGGCTGGCAG	
2 rs2219366	81318138	A	143 84	CACCAACACACATACACATACATT[A/G]TAGCATTTGGAGCTAGAAAAGCT	
10 rs1886951	2425384	A	146 85	CAGCAGCCACTCCTGGCAGAACCCCT[C/T]CTCCCATGCCAGCCACCCCTTGAG	

5.2 Methods of Treatment/Diagnosis

The present invention provides for a method of determining whether or not a human subject is at increased risk for developing ARONJ comprising determining whether nucleic acid, e.g. genomic DNA, of the subject carries an allelic variation or SNP that is a ARONJ biomarker, as described above, for example, by determining the nucleotide sequence of at least a portion of the DNA of the subject and determining whether a variant SNP which is a ARONJ biomarker as set forth above is present, where the presence of said ARONJ biomarker indicates that the subject is at increased risk for developing ARONJ. If a subject is at increased risk of developing ARONJ, the subject may be cautioned/warned to abstain from use of an anti-resorptive agent, such as a BP or Denosumab, avoid dental surgical procedures, or be frequently examined for early detection of ONJ (and then cessation of BP treatment or other therapeutic measures).

In non-limiting embodiments, the present invention provides for a method of determining whether a human subject is at increased risk for developing ARONJ comprising determining whether the genomic DNA of the subject carries an allelic variation of a gene selected from the group consisting of the human RBMS3 gene, the human IGF1R gene, the human IGFBP7 gene, the human DPYD gene, the human ABCC4 gene, or the human GSTM2 gene, where the presence of said allelic variation indicates that the subject is at increased risk for developing ARONJ. In particular non-limiting embodiments, the allelic variations may be in regions or

subregions of those genes as described above, in SNPs represented in TABLES 1, 2 and 3, or in SNPs rs11934877, rs17761305, rs10875055, rs1189437, or rs673151.

In non-limiting embodiments, the present invention provides for a method of determining whether a human subject is at increased risk for developing ARONJ comprising determining whether the genomic DNA of the subject carries a SNPs set forth in TABLE 4 (i.e., any one of SNP ID #40-147 or combinations thereof), where the presence of the indicated allele of the SNP indicates that the subject is at risk for developing ARONJ.

The present invention further provides for a method of treating a human subject suffering from osteoporosis, comprising: (i) determining whether the human subject is at increased risk for developing ARONJ comprising determining whether the genomic DNA of the subject carries an allelic variation that is a ARONJ biomarker, as described above, for example, by determining the nucleotide sequence of at least a portion of the DNA of the subject and determining whether a variant SNP which is a ARONJ biomarker as set forth above is present, where the presence of said ARONJ biomarker indicates that the subject is at increased risk for developing ARONJ; and (ii) if the subject is at increased risk for developing ARONJ, recommending that the subject not be treated with an anti-resorptive agent or be treated with an anti-resorptive agent with relatively lower incidence of ONJ and optionally recommending an alternative treatment for osteoporosis, such as, but not limited to, calcium supplementation, exercise, and/or (iii) if the subject is at increased risk for devel-

oping ARONJ, recommending that the subject not undergo bone invasive dental procedures; and/or (iv) if the biomarker studies suggest that the subject is not at increased risk of ARONJ, initiating or continuing anti-resorptive therapy.

In a non-limiting embodiment, the present invention provides for a method of treating a subject suffering from osteoporosis, comprising obtaining the sequence of a portion of nucleic acid collected from the subject to determine whether the subject carries one or more single nucleotide polymorphism indicative of an increased risk of anti-resorptive therapy-associated osteonecrosis of the jaw selected from the group consisting of the single nucleotide polymorphisms set forth in TABLES 1, 2, 3 4 and combinations thereof, and if the one or more single nucleotide polymorphism is absent, treating the subject with an anti-resorptive agent.

The present invention further provides for a method of treating a human subject suffering from hypercalcemia, comprising: (i) determining whether the human subject is at increased risk for developing ARONJ comprising determining whether the genomic DNA of the subject carries an allelic variant that is a ARONJ biomarker, as described above, for example, by determining the nucleotide sequence of at least a portion of the DNA of the subject and determining whether a variant SNP which is a ARONJ biomarker as set forth above is present, where the presence of said ARONJ biomarker indicates that the subject is at increased risk for developing ARONJ; and (ii) if the subject is at increased risk for developing ARONJ, recommending that the subject be treated with a BP that carries a relatively lower risk of ARONJ or that the subject not be treated with BP and optionally recommending an alternative treatment for hypercalcemia, such as, but not limited to, gallium nitrate, plicamycin (formerly mithramycin), calcitonin, hemodialysis or peritoneal dialysis and/or (iii) if the subject is at increased risk for developing ARONJ, recommending that the subject not undergo bone invasive dental procedures and/or (iv) if the biomarker studies suggest that the subject is not at increased risk of ARONJ, initiating or continuing BP therapy.

In certain non-limiting embodiments, the present invention provides for a method of determining whether a human subject is at increased risk for developing bisphosphonate related osteonecrosis of the jaw comprising determining whether the genomic DNA of the subject carries one or more allelic variation which is a SNP selected from the group consisting of the SNPs set forth in TABLES 1, 2, 3 4 and combinations thereof, where the presence of said allelic variation indicates that the subject is at increased risk for developing ARONJ. In certain non-limiting embodiments, the SNPs include one, two, three or four or at least two, at least three, or at least four of the following: rs17024608 wherein A is substituted by G; rs17761305 wherein C is substituted by T; rs11934877 wherein T is substituted by C; rs10875055 wherein C is substituted by T; rs1189437 wherein A is substituted by C; rs673151, wherein G is substituted by A; and combinations thereof.

5.3 Kits

The present invention provides for kits that may be used to practice the above methods for determining whether the genomic DNA of a subject carries an allelic variation that is a ARONJ biomarker.

In certain non-limiting embodiments of the invention, a kit may comprise one or more primer nucleic acid having a sequence that is complementary to a nucleotide sequence containing or in proximity to the location of a SNP that is a

ARONJ biomarker, as described above. For example, and not by way of limitation, the primer may be extended across the sequence having a SNP.

A "primer" as that term is used herein is a polynucleotide that is at least 8 nucleotides, at least 10 nucleotides, at least 15 nucleotides, at least 20 nucleotides, or at least 25 nucleotides in length (and may be, for example but not limitation, up to 20 nucleotides, up to 30 nucleotides, up to 40 nucleotides, up to 50 nucleotides, up to 100 nucleotides, up to 200 nucleotides, up to 500 nucleotides, up to 1000 nucleotides, in length) and, under reaction conditions, forms a hybrid structure with its target sequence, due to complementarity of at least one sequence in the probe or primer with a sequence in the target sequence. The target sequence, in non-limiting embodiments, may be at least 8 nucleotides, at least 10 nucleotides, at least 15 nucleotides, at least 20 nucleotides, or at least 25 nucleotides in length (and may be, for example but not limitation, up to 20 nucleotides, up to 30 nucleotides, up to 40 nucleotides, up to 50 nucleotides, up to 100 nucleotides, up to 200 nucleotides, up to 500 nucleotides, or up to 1000 nucleotides, in length). In non-limiting embodiments, the primer may be identical to the complement of its target sequence, may be at least 99 percent identical to the complement of its target sequence, may be at least 98 percent identical to the complement of its target sequence, or may be at least 95 percent identical to the complement of its target sequence, and may optionally be fused to a second nucleic acid or other molecule that is non-specific to the subject's nucleic acid but that is used in the detection assay (for example, for purification of extended or amplified primer).

The target sequence may span the location of the SNP or other allelic variation or may be in proximity to it (for example, but not by way of limitation, within up to 20 nucleotides, or up to 50 nucleotides, or up to 100 nucleotides, or up to 200 nucleotides, or up to 500 nucleotides, or up to 1000 nucleotides in genomic DNA or, if the SNP is located in a transcribed region, in RNA or cDNA).

In a specific non-limiting embodiment of the invention, the target sequence of a primer may be within 50 or within 100 nucleotides on either side of (i) the nucleotide that is the location of the SNP or (ii) the other allelic variation, in a genomic DNA, RNA or cDNA sequence.

One primer, as described above, may be used to generate a test fragment by primer extension. Two such primers may be used to generate a test fragment by polymerase chain reaction. The placement of the primer(s) is/are such that the test fragment comprises the location of the SNP or other allelic variation. The resulting test fragment may be sequenced to determine whether a SNP or other allelic variation of the ARONJ biomarker is present.

In non-limiting embodiments, a primer used according to the invention has a target sequence in (or is complementary to at least a portion of or is at least 90 or at least 95 or at least 99 percent homologous to (as determined by standard software such as BLAST or FASTA)) one of SEQ ID Nos 1-85.

In non-limiting embodiments of the invention, primer extension may be used to extend a primer as described above to generate a test fragment that comprises a nucleotide that is the location of a SNP that is a ARONJ biomarker. In non limiting embodiments, the sequence of the test fragment may be determined so as to determine what nucleotide is present at the site of the SNP.

In non-limiting embodiments of the invention, polymerase chain reaction may be used to amplify a test fragment between two primers (as described above), where the test fragment comprises a nucleotide that is the location of a SNP that is a ARONJ biomarker.

In non-limiting embodiments of the invention, a kit may comprise at least one, or at least two, or at least three, or at least four, or at least five, or at least six, or at least seven, or at least eight, or at least nine, or at least ten, and optionally up to five, optionally up to ten, optionally up to twenty, or optionally up to fifty, primer(s) selected from the group of:

primer(s) that may be used to generate test fragments that comprise a nucleotide that is the location of a SNP listed in TABLE 1, or in TABLE 2, or in TABLE 3; or in TABLE 4, and

primer(s) that may be used to generate test fragments that comprise a nucleotide that is the location of a SNP or allelic variation in the human RBMS3 gene, human IGF1R gene, human IGFBP7 gene, human DPYD gene, human ABCC4 gene, or human GSTM2 gene, including the regions and subregions described above, and including the SNPs associated particularly with each of these genes.

In a specific non-limiting embodiment, the kit comprises at least one primer that may be used to generate a test fragment that comprises the nucleotide that is the location of the SNP of rs17024608, namely, the substitution of A by G in SEQ ID NO:1=GATAGAACATAGACTATTGATGTGG AGCATGAG AATTTAAAGTATCTGCA (bolded and underlined), where the presence of a G rather than A is indicative on increased risk of ARONJ, together with a package insert that describes the association between this SNP and ARONJ. Said kit may optionally comprise at least one primer that may be used to generate a test fragment that comprises the nucleotide that is the location of a SNP of a human gene selected from the group consisting of IGF1R, UGFBP7, DPYD, ABCC4, GSTM2, SNP ID #40-147, or combinations thereof. For example, said kit may further comprise at least one primer that may be used to generate a test fragment that comprises the nucleotide that is the location of the SNP of rs17761305 corresponding to position 57934091 of chromosome 4, as represented by the substitution of C by T in SEQ ID NO:20. As another example, said kit may further comprise at least one primer that may be used to generate a test fragment that comprises the nucleotide that is the location of the SNP of rs11934877 corresponding to position 57941026 of chromosome 4, as represented by the substitution of T by C in SEQ ID NO:19.

In certain non-limiting embodiments of the invention a kit as described above comprises primers having, as target sequences, ARONJ biomarkers as set forth above, where said primers for ARONJ biomarkers are at least 20 percent, or at least 30 percent, or at least 40 percent, or at least 50 percent, or at least 60 percent, or at least 70 percent, or at least 80 percent, or at least 90 percent, of the primers present in the kit. In such embodiments, the kit is directed toward detecting ARONJ-associated markers and does not include a majority of primers that are not ARONJ-associated, although primers to serve as controls, for example, may be included (in non-limiting embodiments, the percentage of non-ARONJ associated primers may be up to 50 percent, or up to 40 percent, or up to 30 percent, or up to 20 percent, or up to 10 percent, or up to 5 percent).

In certain non-limiting embodiments, a kit for detecting ARONJ biomarkers may comprise at least one primer that may be used to generate a test fragment that comprises the nucleotide that is the location of the SNP of rs17024608, namely, the substitution of A by G in SEQ ID NO:1=GATAGAACATAGACTATTGATGTGG AATT-TAAAGTATCTGCA (bolded and underlined), where the presence of a G rather than A is indicative on increased risk, together with one or at least one primer for another ARONJ biomarker set forth above.

In certain non-limiting embodiments, a kit for detecting ARONJ biomarkers may comprise at least one primer that may be used to generate a test fragment that comprises the nucleotide that is the location of the SNP of rs17024608, namely, the substitution of A by G in SEQ ID NO:1=GATAGAACATAGACTATTGATGTGG AATT-TAAAGTATCTGCA (bolded and underlined), where the presence of a G rather than A is indicative on increased risk, together with two or at least two primers for other ARONJ biomarkers set forth above, for example, but not limited, to one, two, three or four or at least two, at least three, or at least four of the following: rs17761305 wherein C is substituted by T; rs11934877 wherein T is substituted by C; rs10875055 wherein C is substituted by T; rs1189437 wherein A is substituted by C; rs673151, wherein G is substituted by A; and combinations thereof.

6. EXAMPLE

6.1 Materials and Methods

This research involves an observational, hospital-based, epidemiologic case control study. The research protocol was reviewed and approved by the institutional review boards (IRB) of the participating institutions. Human subject participation required the signing of a written informed consent, as approved by each institution's IRB. The study base of this case control study consisted of individuals who had received bisphosphonates, and who had received care in the clinics of the Massachusetts General Hospital (MGH), the Brigham & Women's Hospital (BWH), the Harvard School of Dental Medicine (HSDM) and its affiliated clinics, and the Nova University Dental School in Florida. In addition to providing their signed consent, individual participants were required to have the ability to answer to a questionnaire, and to provide a saliva sample. No individual was excluded from the study on the basis of gender, religion, political or sexual orientation, or minority group membership.

The identification of cases and controls occurred at the level of the recruiting clinic. Initially, electronic medical records and clinical notes were searched to identify bisphosphonate users. Among the bisphosphonate users, confirmed ONJ cases and unaffected controls were identified and invited to participate in the study by means of an introductory letter. Letters were mailed at the home address of record for all subjects. Three weeks after the initial mailings, a second wave of follow-up letters were sent, followed with telephone calls. Because of multiple co-morbidities, participants were offered the option to participate over the mail or to visit the clinic for an in-person session. Further, research visits were arranged to coincide with scheduled visits in the Oncology wards, when possible. To avoid misclassification of the disease among the controls (avoiding classifying persons with osteonecrosis as unaffected healthy controls) intra-oral examinations were performed on all controls that expressed a willingness to participate. Both cases and controls used the exact same research instrument and same saliva collection method. The research instrument contained questions on the following fields: demographics, including gender, race, ethnicity and availability of medical insurance; recent radiation to the head and neck (a positive answer would exclude them from the study); exposure to risk factors such as tobacco and alcohol use; co-morbidities, including cancer, osteoporosis and various autoimmune diseases; use of certain medications such as steroids, statins or thalidomide; details of their bisphosphonate use; having interventional dental procedures prior to ONJ, such as implant placement or dental extractions; and details on the osteonecrosis of the jaw, including symptom-

tology and recurrence. The saliva collection method utilized the Oragene DNA collection kit (DNA Genotek, Canada).

Following recruitment, the saliva kits were mailed in one batch to the genotyping facility. DNA was extracted following the manufacturer's recommended protocol. High throughput genotyping was performed using the Human Omni Express 12v1.0 Beadchip (Illumina, San Diego) according to the manufacturer's protocol. The Human Omni Express 12v1.0 Beadchip captures 731,442 markers, representing more than 91% of human variation for major alleles with frequencies above 5% in Caucasians.

All genetic data was imported at the Columbia University Medical Center Division of Bio-informatics computer cluster for statistical analysis. After converting the Final Report file format (standard export format from Illumina's GenomeStudio) into ped and map files, all downstream analyses was carried out in PLINK software [5].

To test the quality of the genotyping and to decide the call rate thresholds (both per sample and per marker), the missingness rate was checked by individual and by SNP (locus), respectively. All samples had call rates greater than 95%. 39,456 SNPs with MAF (minor allele frequency) less than 0.01 were excluded as alleles with such low frequency they would have no chance of approaching significance in this study. PLINK was used to test for Hardy Weinberg Equilibrium and SNPs were excluded that deviated from HWE at a $p < 0.0000001$. Cryptic relatedness was tested for by estimating the identity-by-descent (IBD) for all possible pairs of individuals. To estimate the effect of population structure, the smartPCA program from the EIGENSTRAT package (version 3.0) [6] was used to conduct Principal Components Analysis (PCA) in order to expose population structure of the ONJ study group. This process was repeated when looking for additional genetically-matched population controls in publicly available GWAS datasets. Subjects were selected from POPRES [7], Wellcome Trust Case Control Consortium [8], Illumina iControlDB [9], and the international Serious Adverse Events Consortium (iSAEC) [10]. All subjects except the ones from iControlDB were genotyped using Illumina 1M or 1M-duo chips, and the subjects from iControlDB were genotyped using Illumina 500K chip. SNPs from known regions of long-range linkage disequilibrium (LD) [11] were removed before conducting PCA.

The association of single SNPs were tested primarily using logistic regression with the PCA eigen values as covariates under an additive model. The Cochran-Mantel-Haenszel stratified test was also utilized. Both tests take into account the population structure to minimize inflation of test scores. Standard case-control association analyses set the significance p-value at the $p < 5 \times 10^{-8}$ level, with the exception of a candidate gene analysis that used less stringent correction. The candidate gene sub-analysis focused on certain genes that were considered to be of interest, including the Insulin-like Growth Factor (IGF) family, and several ADME genes [12].

Subsequently the genotypes of 30 Caucasian ONJ cases and 1,743 controls from the "extended study group" (described in more detail in the Results section) were imputed using IMPUTE2 [13] (version February 2009), with data from the 1000 Genomes Project (112 individuals, release number March 2010) and HapMap III (June 2010, all ethnicity) as the reference panels. Only the imputed genotypes with posterior probability (reference) of greater than 0.9 were retained. All known SNPs with poor quality were pruned before the imputation to avoid false positives. The genome was divided into 5000 bp length segments and was imputed using ethic mixed panels to increment the quality of the

imputation for rare variants. Stringent QC was carried out on the imputed genotypes. Copy number variations (CNVs) were subsequently inferred from SNP chip data using PennCNV software (April 2009 version) [14]. To ensure the accuracy of CNV calling, stringent sample and CNV filtering procedures were applied. All samples were included that had a LRR standard deviation < 0.5 , maximum number of total CNV calls < 50 , BAF median > 0.55 or < 0.45 , BAF drift > 0.01 or $WF > 0.05$ or < -0.05 (default parameters). Additionally, to ensure high-confidence CNVs, individual CNVs with PennCNV-generated confidence score < 10 ; those with calls based on fewer than 10 SNPs/CNV probes; and those with span within 1 Mb from centromeres or telomeres, were excluded.

6.2 Results

Recruitment. A total of 67 individuals were recruited in the period 2008-09. Of those, 32 were female cases with a mean age of 62.8 years; 15 were female controls with a mean age of 64.8 years; 5 were male controls with a mean age of 63.6 years and 15 were male cases with a mean age of 64.8 years. The majority of the cases (28/47) and controls (13/20) had received zoledronic acid, with an average duration of 22.5 months. The mean months on zoledronic acid was higher in cases than in controls, but the difference was not statistically significant. Similarly, there was no significant difference between cases and controls in mean months on zoledronic acid for the 14 subjects that reported a positive history of osteoporosis. Of the 67 individuals that participated in the study, we were able to extract DNA from 53 samples; 35 patients with osteonecrosis of the jaw and 18 treatment-tolerant controls.

Population structure and selection of genetically matched population controls. In order to identify the ethnicity of the members of the ONJ study group, the genotype data of the original study group, also referred here as "ONJ study group," was combined with that of 987 HapMap III subjects, which include subjects from 11 populations. Six individuals were found to not cluster with the Caucasian (CEU and TSI) HapMap III samples, including three apparent African Americans, one possible Mexican and two subjects with mixed ethnicity. To increase sample size, additional genomic data was introduced for various classes of controls. More specifically, the genotypic results of the 47 Caucasian subjects (cases and controls) in the original study were merged with that of a selected European study group to separate sub-populations among Europeans. The members of the European study group were selected from publicly available datasets genotyped with the Illumina 1M or 1M-duo chips (POPRES, WTCCC and iSAEC study groups), representing sub-populations among Europeans. This analysis showed that the Caucasian subjects clustered with individuals of northwestern, southern and eastern European descent (FIG. 1A-B). Based on the eigen scores of the first two principal components, 1,122 genetically-matched population controls were selected to form the "combined study group".

To further increase the number of genetically matched controls, especially subjects of Eastern European origin, the combined study group was merged with 2,978 Caucasian samples from the iControlDB dataset and PCA was used to cluster all samples together. From this merged study group, the closest controls for each case were selected based on the eigen scores of the first six principal components to form the "extended study group". Finally, the Caucasian ONJ study group was merged with 101 treatment-tolerant cancer subjects from a dataset available via dbGAP to form a "treatment-matched study group" [15] that contains our 30 ONJ cases and a total of 118 treatment-tolerant controls; of the 118

controls, 101 come from the dbGap phs000210.v1 and 17 come from our original ONJ study. Considering recent evidence about the rarity of ONJ, the Extended study group was combined with 27 additional Eastern European subjects taken from phs000210.v1 study group to form the final study group.

Discovery Phase. The Caucasian ONJ study group contains data from 30 Caucasian cases and 17 Caucasian treatment exposed controls. In total, 631,507 SNPs passed quality control. Logistic regression was used to quantify the Odds Ratio and the 95% Confidence Interval of each SNP using the eigen score from the six significant components as covariate to control for population structure. Given the small sample size, single marker association was tested by the Fisher Exact test. TABLE 6, below, summarizes the findings from the genome wide association analysis. This process as repeated comparing the data from the 30 Caucasian cases with various sets of controls, as explained above. Statistical tests of association in all genome-wide association sub-analyses failed to reach statistical significance (genome-wide level of $p < 5 \times 10^{-8}$). Several markers reached borderline significance at the $p < 5 \times 10^{-7}$ level, such as rs8012823 at DPF3; rs11802277 at AL365331.2; rs1075417818.1; rs11189381 at RP11-459F3.3; rs6861122 at AC022120.1; rs4431170 at MARCH1; rs13096022 at GRM7, and several SNPs appeared consistently in the lists of the 10 top associated genes across the various analyses, suggesting possible involvement in the etiology of ONJ. See Appendix for the 10 most associated SNPs of each analysis, along with ORs, p-values, QQ plots and Manhattan plots for each of the different case-control comparisons (caucasian ONJ study group; combined study group; extended study group; treatment matched study group; and, final study group).

Imputation Analysis. Prior to statistical evaluation a quality control routine was followed that included first using the -png-miss option to fill in the missing genotype and then calculating the Average Posterior Probability (APP) of imputed genotypes for each SNP. APP gives a broadly indication of the accuracy of imputed genotypes of a particular SNP. This parameter ranges from 0 to 1, where 1 means the complete certainty of the called genotype. SNPs with APP < 0.9 were discarded. The difference of missingness was tested between cases and controls and the signal intensity was assessed manually using GenomeStudio to access the quality of genotype calls on subjects where the SNPs were genotyped.

Using imputation, 3,542,142 SNPs were analyzed and their association with the risk of ONJ was tested using logistic regression on the extended study group, with six eigenvalues as covariates to control for population structure. Two significant SNPs at the $p < 5 \times 10^{-8}$ level, rs17425952 and rs233723, did not pass quality control, and were therefore discarded as non-significant. One significant SNP was found located in an intron of gene RBMS3, rs17024608, to be associated with an Odds Ratio of 5.4 ($p = 7.5 \times 10^{-8}$). Rs17024608 was present in the genotype data of the combined study group, with a p-value of 7.3×10^{-6} (logistic regression). It was not present in the genotype data of the extended study group because it was pruned for not passing the missing rate threshold ($> 2\%$ of missing data). Rs3821577, the best proxy of rs17024608 on the SNP chips ($r^2 = 0.14$), showed association P-value of $1.0 \times$

10-5 (logistic regression). In the treatment matched study group, rs17024608 showed an association P-value = 1.4×10^{-5} (OR = 5.6, logistic regression). TABLES 7 and 8 summarize the genetic characteristics of rs17024608 and its statistical parameters across the various datasets. FIG. 4 presents the Manhattan plot of the region surrounding the SNP.

CNV Association analysis. Burden and common copy number variants association analyses were performed. Associations were tested using two tails permuted ($\times 10,000$) Fisher's exact test analysis using the PLINK software, by considering duplications and deletions separately. Singleton oversized CNVs larger than 700 kb were investigated to find evidence for individual predisposition to ONJ. All CNVs were excluded that had coverage smaller than 20 genetic markers/CNVs. All analyses were performed on the Caucasian subjects.

After the stringent QC, one subject was excluded from the association analysis. Fifty two individuals (33 cases and 19 controls) passed stringent quality-control criteria for CNV calling; 431 CNVs were called, of which 71 were duplications and 360 were deletions. Cases and controls did not differ significantly in their rate of CNVs for both deletions and duplications. After multi-test correction, none of the common CNVs had a significant association. However, two unique oversized (greater than 700 kb) duplications were found in cases, and none in controls (TABLE 9). The duplications were found on chromosomes 2 (925,407 bp) and 22 (730,236 bp) respectively.

Candidate Genes Analyses. Genes of the IGF gene family and genes related to drug-Absorption, Distribution, Metabolism and Excretion (ADME) were considered of interest at the inception of this study. With regard to the IGF gene family, 1,083 SNPs located within 20 kb of the candidate genes were available in the treatment-matched study group. FIG. 5A shows the QQ-plot for this set of SNPs. The most significantly associated SNPs were rs11934877 (OR 4.128; 95% CI: 1.918-8.885, p-value = 0.0002), intronic to IGFBP7 (FIG. 5B. 2,564 SNPs close to genes related to drug-Absorption, Distribution, Metabolism and Excretion (ADME) [16] were also extracted. FIG. 6A shows the QQ-plot from those SNPs. The most significantly associated SNP was rs10875055 (OR = 4.324; 95% CI: 1.999-9.353, p value = 0.0002001), which is intronic to DPYD (FIG. 6B). The same two panels of markers were retrieved for the extended study group logistic regression results. Data on 867 candidate IGF SNPs and 1,247 ADME SNPs were available for analysis. FIGS. 7A and 8A show QQ plots respectively for the TOP candidate and ADME SNP panels. Top associated candidate SNPs were rs11934877 (OR = 2.95; 95% CI: 1.66-5.25, p-value = 0.00022) intronic close to gene IGFBP7, rs17761305 (OR = 2.88; 95% CI: 1.64-5.07, p value = 0.00023) intergenic SNP close to IGF1R (FIG. 7B). Top associated ADME SNPs were rs1189437 (OR = 4.64; 95% CI: 2.06-10.46, p value = 0.00021), intronic within ABCC4 (FIG. 8B). The same two panels of markers were analyzed in the Final study group (FC) via logistic regression. Data on 967 IGF candidate SNPs and 1,382 ADME SNPs were used. The top associated SNP was rs673151, intronic in GSTM2 gene, with a OR = 3.57; 95% CI: 1.77-7.21, p-value of 0.00035. FIGS. 9 and 10A show QQ plots respectively for the IGF candidate and ADME SNP panels.

TABLE 6

Genome Wide Association Study Results (ten most significant SNPs) for Caucasian ONJ Study Group							
SNP	P	OR (%95)	chrom	Coordinate	type	ancestral allele	closest gene
rs8012823	5.66E-07	0.09 (0.03-0.24)	14	73273544	INTRONIC	T	DPF3
rs11802277	7.38E-07	33 (4.2-257.1)	1	1.18E+08	DOWNSTREAM	G	AL365331.2
rs6900513	1.17E-05	0.12 (0.044-0.32)	6	66333105	INTRONIC	C	EYS
rs10781262	1.80E-05	0.12 (0.046-0.33)	9	77650696	INTERGENIC	A	C9orf41
rs1471646	1.93E-05	11.05 (3.04-40.08)	1	1.99E+08	WITHIN_NON_CODING_GENE	C	RP11-382E9.1
rs4870310	2.29E-05	0.11 (0.040-0.31)	6	1.55E+08	DOWNSTREAM	T	RP11-15G8.1
rs10875148	2.42E-05	23.57 (3.02-183.9)	1	98885908	INTERGENIC	G	AL160056.1
rs4562759	2.65E-05	8.7 (2.95-25.63)	10	83835639	INTRONIC	T	NRG3
rs4878512	2.71E-05	9.16 (2.87-29.26)	9	27630418	INTERGENIC	A	RP11-535I8.1
rs1873291	3.18E-05	0.1423 (0.055-0.36)	6	66344855	INTRONIC	C	EYS

TABLE 7

MAF of rs17024608 among different groups of subjects	
caucasian selection (# samples)	MAF
cases (30)	0.2833
controls (1743)	0.08226
exposed controls (118)	0.06356
EE exposed and general population controls (122)	0.02
EE general population controls	0.015

TABLE 8

OR (CI ± 95) of the top hit in all analyses.			
COHORT	Model	OR 95% CI	P value
EXTENDED (30 vs 1743)	ADD	5.371 (2.8-10.3)	4.25E-07
DRUG EXPOSED (30 vs 112)	ADD	7.102 (2.731-18.47)	5.80E-05
IMPUTATION (30 vs 1743) *	ADD	5.825 (3.065-11.07)	7.47E-08
	DOM	6.483 (2.966-14.17)	2.79E-06
	REC	23.79 (5.518-102.5)	2.13E-05

* On the imputation dataset the association of rs17024608 under dominant and recessive models was tested.

TABLE 9

CVN Details on Large Duplications (found solely in cases)									
FIID	CHR	BP1	BP2	TYPE	SCORE	SITES	length	Start SNP	End SNP
ojn5111	2	132144891	133070297	DUP	53.9	102	925,407	rs850234	rs16837705
ojn1304	22	19063495	19793730	DUP	360.7	205	730,236	rs6003971	rs2845421

6.3 Discussion

Osteonecrosis of the jaw is a serious adverse effect of bisphosphonates, especially among cancer patients on zoledronic acid. For this vulnerable group, osteonecrosis of the jaw adds yet another burden to their already compromised health, negatively affecting their quality of life. A test able to screen subjects for ONJ susceptibility prior to initiating bisphosphonates would have a great clinical utility as it would reduce the incidence of osteonecrosis. The present study identified SNPs in the genes IGF1R, IGFBP7, DPYD, ABCC4, and GSTM2, one or more of which may be used in such a test.

IGFs, especially IGF1 with its tyrosine kinase domain, are growth factors with potent signal transduction capabilities. Insulin like growth factors are molecules with important roles in normal growth and development. IGF1-deficient children fail to achieve appropriate height and pharmacologic thera-

pies now exist to correct such deficiencies [17]. IGF1 and IGF2 are able to influence the replication and differentiation of bone cells through activation of their receptors, especially IGF1R, which plays a role in the cell cycle [18-19]. However, IGF2R seems to have a pro-apoptotic effect since it binds IGF2 and thus reduces available ligand levels for IGF1R [20]. IGF-binding proteins (IGFBPs), produced by bone cells, compete with the receptors in binding the ligands and thus affect the bioavailability of IGF1 and IGF2. IGFBP-4 binds IGFs and blocks their action, whereas IGFBP-5 promotes the stimulatory effects of IGFs [21].

DPYD polymorphisms have been associated with fluorouracil toxicity, especially with bone marrow and gastrointestinal toxicity, mucositis and leucopenia. DPYD has also been linked to autism spectrum disorders, Barrett esophagus and adenocarcinoma [22-24]. A PubMed search on “DPYD gene and bone” or “DPYD gene and necrosis” returned no results; this genotype may be potentially involved in the soft tissue aspect of osteonecrosis’ pathogenesis.

ABCC4, an ATP-binding cassette transporter gene, codes for Multidrug Resistance Protein, (MRP4/ABCC4) a transporter that actively effluxes endogenous and xenobiotic substrates out of cells. Inherited variation in ABC transporters has been associated with the occurrence of serious adverse

effects. For example, ABCC4 has been linked to cyclophosphamide-induced adverse drug reactions in breast cancer patients, especially leucopenia/neutropenia. Currently there is no published information on MRP4 in bone phenotypes. [25-26].

GSTM2 codes for the phase II detoxifying enzyme glutathione-s-transferase, an enzyme that protects cells against toxic insults and enhances cell survival. While a direct effect on bone necrosis has not been described in the published literature, Owur and Kong (Biochem Pharmacol, 2002) have raised the hypothesis that increased concentrations of certain xenobiotics leads to gst-mediated apoptosis, with extreme increases in concentrations leading to rapid cell necrosis. [27] Knowing that bisphosphonates are attracted to areas of active bone loss or trauma, it is then plausible that localized spikes in bisphosphonate concentrations would lead to gst-mediated cell toxicity.

29

The high throughput analysis of the present study was able to identify only one strong signal in RBMS3, and several weak signals in various genes. RBMS3 is a binding protein that belongs to the c-myc family of genes. The protein is located in the cytoplasm and it has two RNA binding domains. It has been shown to bind Prx1, a homeobox transcriptional factor that upregulates collagen 1 [28]. The effect of the specific genotype in the etiology of osteonecrosis is currently unknown; however, it is plausible that RBMS3 rs17024608 may be involved in reduced collagen formation and the disruption of tissue repair.

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Various publications are cited herein, the contents of which are hereby incorporated by reference in their entirieties.

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<210> SEQ ID NO 22
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<212> TYPE: DNA
<213> ORGANISM: Homo sapiens

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<210> SEQ ID NO 23
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US 9,273,357 B2

49**50**

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What is claimed is:

1. A method of treating a human subject suffering from osteoporosis, comprising determining, from a nucleic acid sample from the subject, whether the subject carries single nucleotide polymorphism rs17024608 wherein A is substituted by G, where if the polymorphism is present, the subject is at increased risk for developing bisphosphonate-related osteonecrosis of the jaw relative to a subject that does not carry the polymorphism; and either (i) where the subject carries the polymorphism, treating the subject with an osteoporosis therapy that is an alternative to bisphosphonate treatment and not treating the subject with a bisphosphonate agent or (ii) where the subject does not carry the polymorphism, treating the subject with an osteoporosis therapy that is a bisphosphonate agent.

³⁰ 2. The method of claim 1, where the osteoporosis therapy that is an alternative to bisphosphonate treatment is calcium supplementation.

³⁵ 3. The method of claim 1 where the bisphosphonate agent is selected from the group consisting of alendronate, etidronate, ibadronate, risedronate, pamidronate and zoledronic acid.

⁴⁰ 4. The method of claim 1 where the bisphosphonate agent is selected from the group consisting of pamidronate and zoledronic acid.

5. The method of claim 1 where the bisphosphonate agent is zoledronic acid.

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